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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:58:29 ; Search time 16.704 Seconds
(without alignments)
6907.991 Million cell updates/sec

Title: US-09-698-903B-12
Perfect score: 21
Sequence: 1 gcttgactataatacttgac 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA:*
- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 - 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq:*
 - 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 - 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 - 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 - 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 - 18: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 - 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 - 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 - 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	92.4	21	9	US-09-733-151-12
2	19.4	92.4	21	15	US-10-375-332-12
3	19.4	92.4	694	9	US-09-733-151-39
4	19.4	92.4	694	15	US-10-375-332-39
5	19.4	92.4	831	9	US-09-794-384A-7
6	19.4	92.4	831	17	US-10-801-550-7
7	19.4	92.4	909	9	US-09-733-151-36
8	19.4	92.4	909	15	US-10-375-332-36
9	19.4	92.4	1077	9	US-09-733-151-24
10	19.4	92.4	1077	15	US-10-375-332-24
11	19.4	92.4	4465	13	US-10-047-542-13
12	19.4	92.4	4832	9	US-09-733-151-2

C 13	19.4	92.4	4832	15	US-10-375-332-2	Sequence 2, Appli
C 14	19.4	92.4	4946	9	US-09-733-151-1	Sequence 1, Appli
C 15	19.4	92.4	4946	15	US-10-375-332-1	Sequence 1, Appli
C 16	19.4	92.4	5349	9	US-09-970-921-7	Sequence 7, Appli
C 17	19.4	92.4	6539	9	US-09-509-945-5	Sequence 5, Appli
C 18	19.4	92.4	6548	9	US-09-509-945-4	Sequence 4, Appli
C 19	19.4	92.4	6602	13	US-10-047-542-100	Sequence 100, App
C 20	19.4	92.4	7129	13	US-10-047-542-101	Sequence 101, App
C 21	19.4	92.4	7129	13	US-10-047-542-101	Sequence 101, App
C 22	19.4	92.4	7599	15	US-10-027-880-5	Sequence 5, Appli
C 23	19.4	92.4	8074	13	US-10-047-542-14	Sequence 14, Appli
C 24	19.4	92.4	8340	9	US-09-847-057-4	Sequence 4, Appli
C 25	19.4	92.4	8340	9	US-09-874-926-4	Sequence 4, Appli
C 26	19.4	92.4	9901	10	US-09-940-550A-11	Sequence 11, Appli
C 27	19.4	92.4	10078	13	US-10-033-190-3	Sequence 3, Appli
C 28	19.4	92.4	11978	10	US-09-792-568-8	Sequence 8, Appli
C 29	19.4	92.4	12079	16	US-10-250-821-22	Sequence 22, Appli
C 30	19.4	92.4	12079	16	US-10-250-553-22	Sequence 21, Appli
C 31	19.4	92.4	12085	16	US-10-250-821-21	Sequence 21, Appli
C 32	19.4	92.4	12085	16	US-10-250-553-21	Sequence 20, Appli
C 33	19.4	92.4	12093	16	US-10-250-821-20	Sequence 20, Appli
C 34	19.4	92.4	12093	16	US-10-250-553-20	Sequence 20, Appli
C 35	19.4	92.4	12241	9	US-09-948-138-4	Sequence 4, Appli
C 36	19.4	92.4	12241	13	US-10-033-190-5	Sequence 5, Appli
C 37	19.4	92.4	12241	15	US-10-407-845A-4	Sequence 4, Appli
C 38	19.4	92.4	12438	10	US-09-792-568-9	Sequence 9, Appli
C 39	19.4	92.4	13002	16	US-10-250-821-23	Sequence 23, Appli
C 40	19.4	92.4	13002	16	US-10-250-553-23	Sequence 23, Appli
C 41	19.4	92.4	13905	16	US-10-250-821-24	Sequence 24, Appli
C 42	19.4	92.4	13905	16	US-10-250-553-24	Sequence 24, Appli
C 43	19.4	92.4	15430	16	US-10-250-821-25	Sequence 25, Appli
C 44	19.4	92.4	15430	16	US-10-250-553-25	Sequence 25, Appli
C 45	19.4	92.4	17752	16	US-10-250-821-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1
US-09-733-151-12
; Sequence 12, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: primer 201(BNA01)
US-09-733-151-12

Query Match 92.4%; Score 19.4; DB 9; Length 21;
Best Local Similarity 95.2%; Pred. No. 5.7;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTTGACTATAATACTTGAC 21
Db 1 GCTTGACTATAATACTGAC 21
RESULT 2
US-10-375-332-12

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; Sequence 12, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: primer 201(BNA01)
US-10-375-332-12
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Query Match          92.4%; Score 19.4; DB 15; Length 21;
Best Local Similarity 95.2%; Pred. No. 5.7;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GCTTGGACTATAATACTTGAC 21
   |||||
Db 1 GCTTGGACTATAATACTTGAC 21
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RESULT 3
US-09-733-151-39/c
; Sequence 39, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 39
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(694)
; OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1 in WOSR
US-09-733-151-39
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```
Query Match          92.4%; Score 19.4; DB 9; Length 694;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GCTTGGACTATAATACTTGAC 21
   |||||
Db 694 GCTTGGACTATAATACTTGAC 674
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RESULT 4
US-10-375-332-39/c
; Sequence 39, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
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; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 39
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(694)
; OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1 in WOSR
US-10-375-332-39
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Query Match          92.4%; Score 19.4; DB 15; Length 694;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GCTTGGACTATAATACTTGAC 21
   |||||
Db 694 GCTTGGACTATAATACTTGAC 674
```

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RESULT 5
US-09-794-384A-7
; Sequence 7, Application US/09794384A
; Patent No. US20020144305A1
; GENERAL INFORMATION:
; APPLICANT: Dellaporta, Stephen L.
; APPLICANT: Moreno, Maria A.
; APPLICANT: Yale University
; TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate
; TITLE OF INVENTION: Transmission of a Transgene
; FILE REFERENCE: 44574-5078-US
; CURRENT APPLICATION NUMBER: US/09/794,384A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,524
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: (514)..(813)
US-09-794-384A-7
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Query Match          92.4%; Score 19.4; DB 9; Length 831;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GCTTGGACTATAATACTTGAC 21
   |||||
Db 664 GCTTGGACTATAATACTTGAC 684
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RESULT 6
US-10-801-550-7
; Sequence 7, Application US/10801550
; Publication No. US20040154054A1
; GENERAL INFORMATION:
; APPLICANT: Dellaporta, Stephen L.
; APPLICANT: Moreno, Maria A.
; APPLICANT: Yale University
; TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate
; TITLE OF INVENTION: Transmission of a Transgene
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; FILE REFERENCE: 44574-5078-US
; CURRENT APPLICATION NUMBER: US/10/801,550
; CURRENT FILING DATE: 2004-03-17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(909)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR
US-10-375-332-36

Query Match          92.4%; Score 19.4; DB 15; Length 909;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTTGGACTATAATACCTTGAC 21
        |||
Db       909 GCTTGGACTATAATACCTTGAC 889

RESULT 9
US-09-733-151-24/c
; Sequence 24, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1077)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
US-09-733-151-24

Query Match          92.4%; Score 19.4; DB 9; Length 1077;
Best Local Similarity 95.2%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTTGGACTATAATACCTTGAC 21
        |||
Db       980 GCTTGGACTATAATACCTTGAC 960

RESULT 10
US-10-375-332-24/c
; Sequence 24, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1077

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; FILE REFERENCE: 44574-5078-US
; CURRENT APPLICATION NUMBER: US/10/801,550
; CURRENT FILING DATE: 2004-03-17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(909)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR
US-10-375-332-36/c

Query Match          92.4%; Score 19.4; DB 17; Length 831;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTTGGACTATAATACCTTGAC 21
        |||
Db       664 GCTTGGACTATAATACCTTGAC 684

RESULT 7
US-09-733-151-36/c
; Sequence 36, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(909)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR
US-09-733-151-36

Query Match          92.4%; Score 19.4; DB 9; Length 909;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTTGGACTATAATACCTTGAC 21
        |||
Db       909 GCTTGGACTATAATACCTTGAC 889

RESULT 8
US-10-375-332-36/c
; Sequence 36, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037

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; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1077)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
US-10-375-332-24

Query Match          92.4%; Score 19.4; DB 15; Length 1077;
Best Local Similarity 95.2%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTGGACTATAATACCTGAC 21
Db 980 GCTTGGACTATAATACCTGAC 960

RESULT 11
US-10-047-542-13
; Sequence 13, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.C1P1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 4465
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Expression-type plasmid pBMSP-1
; NAME/KEY: modified_base
; LOCATION: (2150)
; OTHER INFORMATION: a, c, t or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2214)..(2215)
; OTHER INFORMATION: a, c, t or g
US-10-047-542-13

Query Match          92.4%; Score 19.4; DB 13; Length 4465;
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTGGACTATAATACCTGAC 21
Db 3659 GCTTGGACTATAATACCTGAC 3679

RESULT 12
US-09-733-151-2/c
; Sequence 2, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4946
; TYPE: DNA
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; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4832
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4832)
; OTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2

Query Match          92.4%; Score 19.4; DB 9; Length 4832;
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTGGACTATAATACCTGAC 21
Db 163 GCTTGGACTATAATACCTGAC 143

RESULT 13
US-10-375-332-2/c
; Sequence 2, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4832
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4832)
; OTHER INFORMATION: Plasmid pTHW118
US-10-375-332-2

Query Match          92.4%; Score 19.4; DB 15; Length 4832;
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTGGACTATAATACCTGAC 21
Db 163 GCTTGGACTATAATACCTGAC 143
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RESULT 14
US-09-733-151-1/c
; Sequence 1, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4946
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4946)
; OTHER INFORMATION: Plasmid pTHW107
US-09-733-151-1

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Query Match          92.4%; Score 19.4; DB 9; Length 4946;
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1  GCTTGGACTATAATACCTGAC 21
          |||||
Db      163 GCTTGGACTATAATACCTGAC 143

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RESULT 15

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US-10-375-332-1/c
; Sequence 1, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4946
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4946)
; OTHER INFORMATION: Plasmid pTHW107
US-10-375-332-1

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Query Match          92.4%; Score 19.4; DB 15; Length 4946;
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1  GCTTGGACTATAATACCTGAC 21
          |||||
Db      163 GCTTGGACTATAATACCTGAC 143

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Search completed: December 5, 2004, 09:36:24
Job time : 16.704 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 05:20:20 ; Search time 3.528 Seconds
(without alignments)
4230.886 Million cell updates/sec

Title: US-09-698-903B-12
Perfect score: 21
Sequence: 1 gcttgactataatacttgac 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	4	US-09-430-497A-12
2	19.4	92.4	21	4	US-09-457-037B-12
3	19.4	92.4	21	4	US-09-733-151-12
4	19.4	92.4	415	4	US-09-430-497A-8
5	19.4	92.4	416	4	US-09-430-497A-10
6	19.4	92.4	694	4	US-09-457-037B-39
7	19.4	92.4	694	4	US-09-733-151-39
8	19.4	92.4	831	4	US-09-794-384A-7
9	19.4	92.4	909	4	US-09-457-037B-36
10	19.4	92.4	909	4	US-09-733-151-36
11	19.4	92.4	1077	4	US-09-457-037B-24
12	19.4	92.4	1077	4	US-09-733-151-24
13	19.4	92.4	1186	1	US-08-064-121-2
14	19.4	92.4	1186	1	US-08-478-015-2
15	19.4	92.4	1186	3	US-08-475-975-2
16	19.4	92.4	1186	3	US-09-084-889-2
17	19.4	92.4	1303	3	US-08-894-440-2
18	19.4	92.4	1303	3	US-09-458-093-2
19	19.4	92.4	3153	3	US-09-080-625-3
20	19.4	92.4	3153	4	US-09-695-782-3
21	19.4	92.4	3200	1	US-08-453-104-23
22	19.4	92.4	3200	1	US-08-694-824-23
23	19.4	92.4	3201	1	US-08-453-104-22
24	19.4	92.4	3201	2	US-08-694-824-22
25	19.4	92.4	3336	3	US-09-080-625-2
26	19.4	92.4	3336	4	US-09-695-782-2
27	19.4	92.4	3694	3	US-09-080-625-5

28	19.4	92.4	3694	4	US-09-695-782-5
29	19.4	92.4	3877	3	US-09-080-625-4
30	19.4	92.4	3877	4	US-09-695-782-4
31	19.4	92.4	4832	4	US-09-457-037B-2
C	32	19.4	4832	4	US-09-733-151-2
C	33	19.4	4946	3	US-08-817-188-1
C	34	19.4	4946	4	US-09-457-037B-1
C	35	19.4	4946	4	US-09-733-151-1
C	36	19.4	5349	3	US-09-068-101-7
C	37	19.4	5349	4	US-09-970-921-7
C	38	19.4	5560	3	US-08-817-188-5
C	39	19.4	5564	3	US-08-894-440-4
C	40	19.4	5864	3	US-08-894-440-4
C	41	19.4	5864	3	US-09-458-093-4
C	42	19.4	5864	3	US-09-458-093-4
C	43	19.4	5865	4	US-09-430-497A-1
C	44	19.4	5865	4	US-09-430-497A-1
45	19.4	92.4	6548	3	US-08-694-440-1

ALIGNMENTS

RESULT 1

US-09-430-497A-12
; Sequence 12, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BRUCKELBER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430,497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: MDB201
US-09-430-497A-12

Query Match	100.0%	Score 21;	DB 4;	Length 21;
Best Local Similarity	100.0%	Pred. No. 0.1;		
Matches	21;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;
Qy	1	GCTTGACTATATACTTGAC	21	
Db	1	GCTTGACTATATACTTGAC	21	

RESULT 2

US-09-457-037B-12
; Sequence 12, Application US/09457037B
; Patent No. 6506963
; GENERAL INFORMATION:
; APPLICANT: De Boch, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/457,037B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: primer 201(BNA01)
US-09-457-037B-12

Query Match      92.4%; Score 19.4; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTGGACTATAATACCTTGAC 21
Db 1 GCTTGGACTATAATACCTTGAC 21

RESULT 3
US-09-733-151-12
; Sequence 12, Application US/09733151
; Patent No. 6563026
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: primer 201(BNA01)
US-09-733-151-12

Query Match      92.4%; Score 19.4; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTGGACTATAATACCTTGAC 21
Db 1 GCTTGGACTATAATACCTTGAC 21

RESULT 4
US-09-430-497A-8/c
; Sequence 8, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BEUCKELEER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430,497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5' border
; OTHER INFORMATION: flanking region of elite event MS-B2
; NAME/KEY: misc_feature
; LOCATION: (1)..(234)
; OTHER INFORMATION: plant DNA
; NAME/KEY: misc_feature
; LOCATION: (235)..(415)

; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: primer 201(BNA01)
US-09-457-037B-12

Query Match      92.4%; Score 19.4; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTGGACTATAATACCTTGAC 21
Db 1 GCTTGGACTATAATACCTTGAC 21

RESULT 3
US-09-733-151-12
; Sequence 12, Application US/09733151
; Patent No. 6563026
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: primer 201(BNA01)
US-09-733-151-12

Query Match      92.4%; Score 19.4; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTGGACTATAATACCTTGAC 21
Db 1 GCTTGGACTATAATACCTTGAC 21

RESULT 4
US-09-430-497A-8/c
; Sequence 8, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BEUCKELEER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430,497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5' border
; OTHER INFORMATION: flanking region of elite event MS-B2
; NAME/KEY: misc_feature
; LOCATION: (1)..(234)
; OTHER INFORMATION: plant DNA
; NAME/KEY: misc_feature
; LOCATION: (235)..(415)

; NAME/KEY: misc_feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: primer 201(BNA01)
US-09-457-037B-12

Query Match      92.4%; Score 19.4; DB 4; Length 415;
Best Local Similarity 95.2%; Pred. No. 0.9;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTGGACTATAATACCTTGAC 21
Db 335 GCTTGGACTATAATACCTTGAC 315

RESULT 5
US-09-430-497A-10
; Sequence 10, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BEUCKELEER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430,497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 3' border
; OTHER INFORMATION: flanking region of elite event MS-B2
; NAME/KEY: misc_feature
; LOCATION: (1)..(193)
; OTHER INFORMATION: T-DNA
; NAME/KEY: misc_feature
; LOCATION: (194)..(416)
; OTHER INFORMATION: plant DNA
US-09-430-497A-10

Query Match      92.4%; Score 19.4; DB 4; Length 416;
Best Local Similarity 95.2%; Pred. No. 0.9;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTGGACTATAATACCTTGAC 21
Db 81 GCTTGGACTATAATACCTTGAC 101

RESULT 6
US-09-457-037B-39/c
; Sequence 39, Application US/09457037B
; Patent No. 6506963
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/457,037B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(694)
; OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1 in WOSR
US-09-457-037B-39
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Query Match 92.4%; Score 19.4; DB 4; Length 694;
Best Local Similarity 95.2%; Pred. No. 0.94; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1 GCTTGGACTATAAATCTTGAC 21
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Db 694 GCTTGGACTATAAATCTTGAC 674
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RESULT 7
US-09-733-151-39/c
; Sequence 39, Application US/09733151
; Patent No. 6563026
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(694)
; OTHER INFORMATION: sequence comprising the 5' flanking region of RP-BN1 in WOSR
US-09-733-151-39

Query Match 92.4%; Score 19.4; DB 4; Length 694;
Best Local Similarity 95.2%; Pred. No. 0.94; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1 GCTTGGACTATAAATCTTGAC 21
|||||
Db 694 GCTTGGACTATAAATCTTGAC 674
|||||

RESULT 8
US-09-794-384A-7
; Sequence 7, Application US/09794384A
; Patent No. 6743968
; GENERAL INFORMATION:
; APPLICANT: Dellaporta, Stephen L.
; APPLICANT: Moreno, Maria A.
; APPLICANT: Yale University
; TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate
; FILE REFERENCE: 44574-5078-US
; CURRENT APPLICATION NUMBER: US/09/794,384A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,524
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: (514)..(813)
US-09-794-384A-7

Query Match 92.4%; Score 19.4; DB 4; Length 831;
Best Local Similarity 95.2%; Pred. No. 0.96; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1 GCTTGGACTATAAATCTTGAC 21
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Db 664 GCTTGGACTATAAATCTTGAC 684
|||||

RESULT 9
US-09-457-037B-36/c
; Sequence 36, Application US/09457037B
; Patent No. 6506963
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/457,037B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(909)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR
US-09-457-037B-36

Query Match 92.4%; Score 19.4; DB 4; Length 909;
Best Local Similarity 95.2%; Pred. No. 0.97; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1 GCTTGGACTATAAATCTTGAC 21
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Db 909 GCTTGGACTATAAATCTTGAC 889
|||||

RESULT 10
US-09-733-151-36/c
; Sequence 36, Application US/09733151
; Patent No. 6563026
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(909)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR
US-09-733-151-36

Query Match 92.4%; Score 19.4; DB 4; Length 909;
Best Local Similarity 95.2%; Pred. No. 0.97; Mismatches 1; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1 GCTTGGACTATAAATCTTGAC 21
|||||
Db 909 GCTTGGACTATAAATCTTGAC 889
|||||

RESULT 11
US-09-457-037B-24/c

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/ Sequence 24, Application US/09457037B
/ Patent No. 6506963
/ GENERAL INFORMATION:
/ APPLICANT: De Borch, et al.
/ TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
/ FILE REFERENCE: 514412-2019
/ CURRENT APPLICATION NUMBER: US/09/457,037B
/ CURRENT FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: 09/457,037
/ PRIOR FILING DATE: 1999-12-08
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 24
/ LENGTH: 1077
/ TYPE: DNA
/ ORGANISM: Brassica napus
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(1077)
/ OTHER INFORMATION: sequence comprising the 5' flanking region of RP-BN1
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(45)
/ OTHER INFORMATION: pGEM-T vector
/ US-09-457-037B-24

Query Match          92.4%; Score 19.4; DB 4; Length 1077;
Best Local Similarity 95.2%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTTGGACTATAATCTTGAC 21
Db      980 GCTTGGACTATAATCTTGAC 960

RESULT 12
US-09-733-151-24/c
/ Sequence 24, Application US/09733151
/ Patent No. 6563026
/ GENERAL INFORMATION:
/ APPLICANT: De Borch, et al.
/ TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
/ FILE REFERENCE: 514412-2019
/ CURRENT APPLICATION NUMBER: US/09/733,151
/ CURRENT FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: 09/457,037
/ PRIOR FILING DATE: 1999-12-08
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 24
/ LENGTH: 1077
/ TYPE: DNA
/ ORGANISM: Brassica napus
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(1077)
/ OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
/ US-09-733-151-24

Query Match          92.4%; Score 19.4; DB 4; Length 1077;
Best Local Similarity 95.2%; Pred. No. 0.99;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTTGGACTATAATCTTGAC 21
Db      980 GCTTGGACTATAATCTTGAC 960

RESULT 13
US-08-064-121-2
/ Sequence 2, Application US/08064121
/ Patent No. 5641664
/ GENERAL INFORMATION:
/ APPLICANT: D'HALLUIN, Kathleen
```

```
/ APPLICANT: GOBEL, Elke
/ TITLE OF INVENTION: PROCESS FOR TRANSFORMING
/ TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Burns, Doane, Swecker & Mathis
/ STREET: George Mason Bldg., Washington & Prince Sts.
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/064,121
/ FILING DATE: 24-MAY-1993
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 90403332.1
/ FILING DATE: 23-NOV-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: EP 91401888.2
/ FILING DATE: 08-JUL-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Crane-Feury, Sharon E
/ REGISTRATION NUMBER: 36,113
/ REFERENCE/DOCKET NUMBER: 010830-043
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-8620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1186 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: probe
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/ NAME/KEY: -
/ LOCATION: 1..8
/ OTHER INFORMATION: /note= "sequence derived from
/ OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 9..790
/ OTHER INFORMATION: /label= NPTII
/ OTHER INFORMATION: /note= "coding sequence of neomycine
/ OTHER INFORMATION: phosphotransferase gene"
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 791..1186
/ OTHER INFORMATION: /label= 3'g7
/ OTHER INFORMATION: /note= "3' regulatory sequence containing the
/ OTHER INFORMATION: polyadenylation site derived from Agrobacterium
/ OTHER INFORMATION: T-DNA gene 7"
/ US-08-064-121-2

Query Match          92.4%; Score 19.4; DB 1; Length 1186;
Best Local Similarity 95.2%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTTGGACTATAATCTTGAC 21
Db      1113 GCTTGGACTATAATCTTGAC 1133
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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTGGACTATAACTTGAC 21
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 Db 1113 GCTTGGACTATAACTTGAC 1133

RESULT 15
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 ; Sequence 2, Application US/08475975
 ; Patent No. 6002070
 ; GENERAL INFORMATION:
 ; APPLICANT: D'HALLUIN, Kathleen
 ; APPLICANT: GOBEL, Elke
 ; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
 ; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: George Mason Bldg., Washington & Prince Sts.
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/475,975
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,121
 ; FILING DATE: 24-MAY-1993
 ; APPLICATION NUMBER: EP 90403332.1
 ; FILING DATE: 23-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 91401888.2
 ; FILING DATE: 08-JUL-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crane-Feury, Sharon E
 ; REGISTRATION NUMBER: 36,113
 ; REFERENCE/DOCKET NUMBER: 010830-043
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1186 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: probe
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 1..8
 ; OTHER INFORMATION: /note= "sequence derived from
 ; OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 791..1186
 ; OTHER INFORMATION: /label= NPTII
 ; OTHER INFORMATION: /note= "coding sequence of neomycine
 ; OTHER INFORMATION: phosphotransferase gene"
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 791..1186

RESULT 14
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 ; Sequence 2, Application US/08478015
 ; Patent No. 5712135
 ; GENERAL INFORMATION:
 ; APPLICANT: D'HALLUIN, Kathleen
 ; APPLICANT: GOBEL, Elke
 ; TITLE OF INVENTION: PROCESS FOR TRANSFORMING
 ; TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/478,015
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 90403332.1
 ; FILING DATE: 23-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 91401888.2
 ; FILING DATE: 08-JUL-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/064,121
 ; FILING DATE: 23-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McGowan, Malcolm K.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 010830-088
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1186 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: probe
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 1..8
 ; OTHER INFORMATION: /note= "sequence derived from
 ; OTHER INFORMATION: tapetum specific promoter of Nicotiana tabacum"
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 9..790
 ; OTHER INFORMATION: /label= NPTII
 ; OTHER INFORMATION: /note= "coding sequence of neomycine phosphotransferase gene"
 ; FEATURE:
 ; NAME/KEY: -
 ; LOCATION: 791..1186
 ; OTHER INFORMATION: /label= 3'g7
 ; OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
 ; OTHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"
 ; OTHER INFORMATION:
 ; US-08-478-015-2

Query Match 92.4%; Score 19.4; DB 1; Length 1186;
 Best Local Similarity 95.2%; Pred. No. 1;

; OTHER INFORMATION: /label= 3'g7
; OTHER INFORMATION: /note= "3' regulatory sequence containing the
; OTHER INFORMATION: polyadenylation site derived from Agrobacterium
; OTHER INFORMATION: T-DNA gene 7"
US-08-475-975-2

Query Match 92.4%; Score 19.4; DB 3; Length 1186;
Best Local Similarity 95.2%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTGGACTATATCTTGCAC 21
Db 1113 GCTTGGACTATATCTTGCAC 1133

Search completed: December 5, 2004, 07:17:54
Job time : 4.528 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:58:29 ; Search time 18.2949 Seconds
(without alignments)
6907.991 Million cell updates/sec

Title: US-09-698-903B-11

Perfect score: 23

Sequence: 1 gaaatccatgtaagcagcagg 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
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- 19: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	18.8	81.7	173	10	US-09-923-876-5059
C 3	18.4	80.0	572	13	US-10-027-632-239504
C 4	18.4	80.0	572	13	US-10-027-632-239505
C 5	18.4	80.0	572	15	US-10-027-632-239504
C 6	18.4	80.0	572	15	US-10-027-632-239505
C 7	18.4	80.0	16570	16	US-10-275-287-2
C 8	18.2	79.1	478	9	US-09-864-761-11151
C 9	17.4	75.7	628	13	US-10-027-632-143567
C 10	17.4	75.7	628	15	US-10-027-632-143567
C 11	17.4	75.7	1728	13	US-10-027-632-97618
C 12	17.4	75.7	1728	13	US-10-027-632-97619

C 13	17.4	75.7	1728	15	US-10-027-632-97618
C 14	17.4	75.7	1728	15	US-10-027-632-97619
C 15	17.4	75.7	90541	9	US-09-759-359A-3
C 16	17.4	75.7	90541	15	US-10-207-973-3
C 17	17.4	75.7	90541	17	US-10-798-676-3
C 18	17.2	74.8	468	10	US-09-918-595-3102
C 19	17.2	74.8	844	13	US-10-027-632-144465
C 20	17.2	74.8	844	15	US-10-027-632-144465
C 21	17.2	74.8	850	15	US-10-369-493-30363
C 22	17.2	74.8	1677	18	US-10-425-115-28599
C 23	17.2	74.8	2016	15	US-10-094-749-1146
C 24	17.2	74.8	2070	17	US-10-437-963-27021
C 25	17.2	74.8	2255	9	US-09-933-825-4
C 26	17.2	74.8	3987	14	US-10-198-846-12468
C 27	17.2	74.8	4156	15	US-10-158-034-31
C 28	17.2	74.8	4495	15	US-10-037-270-352
C 29	17.2	74.8	4495	15	US-10-117-722-352
C 30	17.2	74.8	9274	9	US-09-885-535-3
C 31	17.2	74.8	32205	15	US-10-158-034-116
C 32	17.2	74.8	256493	13	US-10-087-192-1000
C 33	17.2	73.9	1190	13	US-10-027-632-261250
C 34	17.2	73.9	1190	13	US-10-027-632-261251
C 35	17.2	73.9	1190	15	US-10-027-632-261250
C 36	17.2	73.9	1190	15	US-10-027-632-261251
C 37	16.8	73.0	363	16	US-10-057-475B-10553
C 38	16.8	73.0	363	16	US-10-154-884B-10553
C 39	16.8	73.0	502	17	US-10-021-323-7417
C 40	16.8	73.0	504	17	US-10-021-323-7468
C 41	16.8	73.0	552	16	US-10-424-599-100955
C 42	16.8	73.0	1354	17	US-10-437-963-91169
C 43	16.8	73.0	1592	17	US-10-437-963-60332
C 44	16.8	73.0	2427	17	US-10-437-963-79891
C 45	16.8	73.0	10514	9	US-09-764-877-3470

ALIGNMENTS

RESULT 1

US-09-923-876-5059/c
; Sequence 5059, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalngudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 5059
; LENGTH: 173
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456286H1
; NAME/KEY: unsure
; LOCATION: 58 115, 143
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5059

Query Match 81.7%; Score 18.8; DB 9; Length 173;
Best Local Similarity 87.0%; Pred. No. 63;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GAAATCCATGTAAGCAGCAGGG 23

Db
129 GACATCCATGTAAACNCAGCAGG 107

RESULT 2

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US-09-923-876-5059/c
/ Sequence 5059, Application US/09923876
/ Publication No. US20030237110A9
/ GENERAL INFORMATION:
/ APPLICANT: Lalgudi, Raghunath V.
/ APPLICANT: Kamicaki, Laura Y. (Ito)
/ APPLICANT: Sherman, Bradley K.
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
/ FILE REFERENCE: PL-0012-1 CON
/ CURRENT APPLICATION NUMBER: US/09/923,876
/ CURRENT FILING DATE: 2001-08-06
/ PRIOR APPLICATION NUMBER: 09/298,329
/ PRIOR FILING DATE: 1999-04-21
/ PRIOR APPLICATION NUMBER: 60/085,331
/ PRIOR FILING DATE: 1998-05-05
/ NUMBER OF SEQ ID NOS: 6332
/ SOFTWARE: PERL Program
/ SEQ ID NO 5059
/ LENGTH: 173
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: Incyte ID No. US20030237110A9 700456286H1
/ NAME/KEY: unsure
/ LOCATION: 58, 115, 143
/ OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5059

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Query Match 81.7%; Score 18.8; DB 10; Length 173;
Best Local Similarity 87.0%; Pred.No. 63;
Matches 20; Conservative 0; Mismatches 3; Indels 0

Qy 1 GAAATCCATGTAAAGCAGCAGG 23
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Db 129 GACATCCATGTAAACNCAGCAGG 107

RESULTS. T 3

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1  RESULT 3
2  US-10-027-632-239504/c
3  ; Sequence 239504, Application US/10027632
4  ; Publication No. US0020198371A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Wang, David G.
7  ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
8  ; POLYMORPHISMS IN THE HUMAN GENOME
9  ; FILE REFERENCE: 108847.129
10 ; CURRENT APPLICATION NUMBER: US/10/027,632
11 ; CURRENT FILING DATE: 2002-04-30
12 ; PRIOR APPLICATION NUMBER: US 60/218,006
13 ; PRIOR FILING DATE: 2000-07-12
14 ; PRIOR APPLICATION NUMBER: US 60/198,676
15 ; PRIOR FILING DATE: 2000-04-20
16 ; PRIOR APPLICATION NUMBER: US 60/193,483
17 ; PRIOR FILING DATE: 2000-03-29
18 ; PRIOR APPLICATION NUMBER: US 60/185,218
19 ; PRIOR FILING DATE: 2000-02-24
20 ; PRIOR APPLICATION NUMBER: US 60/167,363
21 ; PRIOR FILING DATE: 1999-11-23
22 ; PRIOR APPLICATION NUMBER: US 60/156,358
23 ; PRIOR FILING DATE: 1999-09-28
24 ; PRIOR APPLICATION NUMBER: US 60/146,002
25 ; PRIOR FILING DATE: 1999-08-09
26 ; NUMBER OF SEQ ID NOS: 325720
27 ; SOFTWARE: FastSeq for Windows Version 4.0
28 ; SEQ ID NO 239504
29 ; LENGTH: 572
30 ; TYPE: DNA

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; ORGANISM: Human
US-10-027-632-239504

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Query Match      80.0%; Score 18.4; DB 13; Length 572;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0
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Qy 2 AAATCCATGTAAGCAGCAG 21
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RESULT 4

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US-10-027-632-239505/c
/ Sequence 239505, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ POLYMORPHISMS IN THE HUMAN GENOME
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: fastseq for Windows Version 4.0
/ SEQ ID NO 239505
/ LENGTH: 572
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-239505

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Query Match      80.0%; Score 18.4; DB 13; Length 572;
Best Local Similarity 95.0%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2 AAATCCATGTAAGCAGCAG 21
Db 369 AAAGCCATGTAAGCAGCAG 350

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US-10-027-632-239504/c
; Sequence 239504, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24

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NO.	TITLE OF INVENTION:	RECOMBINANT VECTORS CONTAINING INTERGENOUS HUMAN CYTOMEGALOVIRUS
1	TITLE OF INVENTION:	with preserved wild-type characteristics of clinical isolates

; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408

APPLICANT: Hahn, Gabriele

APPLICANT ;

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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11151
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005083.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.43
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6
US-09-864-761-11151

Query Match 79.1%; Score 18.2; DB 9; Length 478;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGGACGAGG 23
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Db 316 GACATCCATGTAAGGACGAGG 294

RESULT 9
US-10-027-632-143567
; Sequence 143567, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143567
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-143567

Query Match 75.7%; Score 17.4; DB 13; Length 628;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATCCATGTAAGGACGAGG 22
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Db 597 ATCCATGTAAGGACGAGG 615

RESULT 10
US-10-027-632-143567
; Sequence 143567, Application US/10027632
; Publication No. US20030204075A9

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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
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; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143567
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-143567

Query Match 75.7%; Score 17.4; DB 15; Length 628;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATCCATGTAAGGACGAGG 22
|||
Db 597 ATCCATGTAAGGACGAGG 615

RESULT 11
US-10-027-632-97618/c
; Sequence 97618, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97618
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-97618

Query Match 75.7%; Score 17.4; DB 13; Length 1728;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAAATCCATGTAAGCACC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1710 GAAATCCATGTAAGCACC 1692

RESULT 12

US-10-027-632-97619/c
; Sequence 97619, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97619
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-97619

Query Match 75.7%; Score 17.4; DB 13; Length 1728;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGCACC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1710 GAAATCCATGTAAGCACC 1692

RESULT 13

US-10-027-632-97618/c
; Sequence 97618, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97618
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-97618

Query Match 75.7%; Score 17.4; DB 15; Length 1728;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGCACC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1710 GAAATCCATGTAAGCACC 1692

RESULT 14

US-10-027-632-97619/c
; Sequence 97619, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97619
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-97619

Query Match 75.7%; Score 17.4; DB 15; Length 1728;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGCACC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1710 GAAATCCATGTAAGCACC 1692

RESULT 15

US-09-759-359A-3
; Sequence 3, Application US/09759359A
; Patent No. US20020094560A1
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-3

Query Match      75.7%; Score 17.4; DB 9; Length 90541;
Best Local Similarity 94.7%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATCCATGTAAAGCAGCAG 21
        |||||
Db      66140 ATCCATGTAAAGCAGCAG 66158

Search completed: December 5, 2004, 09:36:24
Job time : 20.2949 secs
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ALIGNMENTS

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Query Match      100.0%; Score 23; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 23: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-430-497A-8
; Sequence 8, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BEUCKELEER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430.497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	23	100.0	23	4	US-09-430-457A-11	Sequence 11, Appl
2	23	100.0	415	4	US-09-430-457A-8	Sequence 8, Appl
3	23	100.0	416	4	US-09-430-457A-10	Sequence 10, Appl
C	17.4	75.7	90541	4	US-09-753-359A-3	Sequence 3, Appl
5	17.4	75.7	90541	4	US-10-207-973-3	Sequence 3, Appl
C	17.2	74.8	1909	4	US-09-270-767-13425	Sequence 13425, A
7	17.2	74.8	4495	4	US-09-620-312D-352	Sequence 352, A
C	17.2	74.8	8874	3	US-08-894-344C-1	Sequence 1, Appl
8	17.2	74.8	8874	3	US-09-128-028-1	Sequence 1, Appl
C	17.2	74.8	9621	3	US-09-720-655B-3	Sequence 3, Appl
9	16.6	72.2	292	4	US-09-621-976-3416	Sequence 1416, Ap
C	16.6	72.2	404	4	US-09-621-976-15579	Sequence 15579, A
11	16.6	72.2	446	4	US-09-621-976-181	Sequence 181, App
C	16.6	72.2	542	4	US-09-107-532A-2051	Sequence 2051, Ap
13	16.6	72.2	1416	4	US-09-673-395A-3	Sequence 3, Appl
C	16.6	72.2	1571	4	US-09-023-655-353	Sequence 253, App
15	16.6	72.2	1791	4	US-09-720-655B-8	Sequence 8, Appl
C	16.6	72.2	1833	4	US-08-964-127-1	Sequence 1, Appl
17	16.6	72.2	2460	3	US-09-496-692-1	Sequence 1, Appl
C	16.6	72.2	2460	3	US-10-000-273-1	Sequence 1, Appl
19	16.6	72.2	2460	4	US-09-238-303-7	Sequence 7, Appl
C	16.6	72.2	9751	3	US-09-946-239-7	Sequence 7, Appl
21	16.6	72.2	9751	4	US-09-747-259-11	Sequence 11, Appl
22	16.4	71.3	1515	4	US-09-593-360B-56	Sequence 56, Appl
23	16.4	71.3	1701	4	US-09-978-594-762	Sequence 762, App
24	16.4	71.3	2171	4	US-09-913-039-293	Sequence 293, App
25	16.4	71.3	5105	4	US-08-833-399-9	Sequence 9, Appl
26	16.4	71.3	5105	3		
27	16.2	70.4	27	3		

; OTHER INFORMATION: Description of Artificial Sequence: 5' border
; NAME/KEY: misc.feature
; LOCATION: (1)..(234)
; OTHER INFORMATION: plant DNA
; NAME/KEY: misc.feature
; LOCATION: (235)..(415)
; OTHER INFORMATION: T-DNA
US-09-430-497A-8

Query Match 100.0%; Score 23; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGCAGCAGG 23
Db 152 GAAATCCATGTAAGCAGCAGG 174

RESULT 3
US-09-430-497A-10/c
; Sequence 10, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BEUCKELEER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430,497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 3' border
; NAME/KEY: misc.feature
; LOCATION: (1)..(193)
; OTHER INFORMATION: T-DNA
; NAME/KEY: misc.feature
; LOCATION: (194)..(416)
; OTHER INFORMATION: plant DNA
US-09-430-497A-10

Query Match 100.0%; Score 23; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGCAGCAGG 23
Db 263 GAAATCCATGTAAGCAGCAGG 241

RESULT 4
US-09-759-359A-3
; Sequence 3, Application US/09759359A
; Patent No. 6492153
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541

; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-3

Query Match 75.7%; Score 17.4; DB 4; Length 90541;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AATCCATGTAAGCAGCAG 21
Db 66140 AATCCATGTAAGCAGCAG 66158

RESULT 5
US-10-207-973-3
; Sequence 3, Application US/10207973
; Patent No. 6753175
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-10-207-973-3

Query Match 75.7%; Score 17.4; DB 4; Length 90541;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AATCCATGTAAGCAGCAG 21
Db 66140 AATCCATGTAAGCAGCAG 66158

RESULT 6
US-09-270-767-13425/c
; Sequence 13425, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7328-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13425
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13425

Query Match 74.8%; Score 17.2; DB 4; Length 1909;
Best Local Similarity 86.4%; Pred. No. 65;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAATCCATGTAAGCAGCAGG 23
Db 293 AAATTCATCTCAAGCAGCAGG 272

RESULT 7
US-09-620-312D-352
; Sequence 352, Application US/09620312D
; Patent No. 6569662

GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyang
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 352
LENGTH: 4495
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (307)..(3006)
US-09-620-312D-352

Query Match 74.8%; Score 17.2; DB 4; Length 4495;
Best Local Similarity 86.4%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAATCCATGTTAAAGCAGCAGG 23
Db 3034 AACTCTTGTAAAGCAGCAGG 3055

RESULT 8
US-08-894-344C-1/c
Sequence 1, Application US/08894344C
Patent No. 6172196
GENERAL INFORMATION:
APPLICANT: KAWASAKI, Hideki
APPLICANT: TOKAI, Masaya
APPLICANT: KIKUCHI, Yasuhiro
APPLICANT: OUCHI, Koza
TITLE OF INVENTION: DNA ENCODING PROTEIN COMPLEMENTING
TITLE OF INVENTION: YEAST
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1440 Kb storage.
COMPUTER: IBM PS/V
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,344C
FILING DATE: 15-AUGUST-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP343700/95
FILING DATE: 28-DECEMBER-1995
APPLICATION NUMBER: PCT/JP96/03862
FILING DATE: 27-DECEMBER-1996
ATTORNEY/AGENT INFORMATION:
NAME: Perry, Lawrence S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-2100
TELEFAX: 212-218-2200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 874 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
STRAIN: X2180-1B
FEATURE:
NAME/KEY: CDS
LOCATION: 1 to 874
IDENTIFICATION METHOD: E
FEATURE:
NAME/KEY: cleavage-site
LOCATION: 1291 to 1296
IDENTIFICATION METHOD: S
FEATURE:
NAME/KEY: cleavage-site
LOCATION: 5927 to 5032
IDENTIFICATION METHOD: S
FEATURE:
NAME/KEY: cleavage-site
LOCATION: 4388 to 4393
IDENTIFICATION METHOD: S
FEATURE:
NAME/KEY: cleavage-site
LOCATION: 7675 to 7680
IDENTIFICATION METHOD: S
US-08-894-344C-1

Query Match 74.8%; Score 17.2; DB 3; Length 8874;
Best Local Similarity 86.4%; Pred. No. 92;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAATCCATGTTAAAGCAGCAGG 23
Db 7552 AAATTAATGTAAGCACCAGG 7531

RESULT 9
US-09-125-028-1/c
Sequence 1, Application US/09125028A
Patent No. 6190707
GENERAL INFORMATION:
APPLICANT: WADOUX, Isabelle
APPLICANT: COLAVITZA, Didier
APPLICANT: LOIEZ, Annie
TITLE OF INVENTION: NOVEL COLD-SENSITIVE BREAD-MAKING YEASTS
FILE REFERENCE: levure sensible froid
CURRENT APPLICATION NUMBER: US/09/125,028A
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: PCT/FR97/00254
EARLIER FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 9621
TYPE: DNA

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; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9318)
; OTHER INFORMATION: Use of n signifies any of g, a, c or t
US-09-125-028-1

Query Match      74.8%; Score 17.2; DB 3; Length 9621;
Best Local Similarity 86.4%; Pred. No. 94;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAATCCATGTAAGCAGCAGGG 23
Db 7927 AAATTAATGTAAGCAGCAGGG 7906

RESULT 10
US-09-720-655B-3/c
; Sequence 3, Application US/09720655B
; Patent No. 6723521
; GENERAL INFORMATION:
; APPLICANT: YOSHIMOTO, MAKOTO
; APPLICANT: YAZAKI, MADOKA
; APPLICANT: MATSUMOTO, KAYO
; APPLICANT: TAKAYAMA, KIYOSHI
; APPLICANT: TSURITANI, KATSUKI
; TITLE OF INVENTION: SUGAR TRANSPORTER
; FILE REFERENCE: ASA-C034
; CURRENT APPLICATION NUMBER: US/09/720,655B
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: JP 10/187235
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 292
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (36)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (47)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (251)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (273)
; OTHER INFORMATION: a, c, g, t, unknown or other
US-09-720-655B-3

Query Match      72.2%; Score 16.6; DB 4; Length 292;
Best Local Similarity 82.6%; Pred. No. 83;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGCAGCAGGG 23
Db 128 GAAGTGAATGTAAGCAGCAGGG 106

RESULT 11
US-09-621-976-1416/c
; Sequence 1416, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 67..390
; NAME/KEY: sig_peptide
; LOCATION: 67..126
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 8.39999961853027
; OTHER INFORMATION: seq AVVGCLLVPPAER/NK
US-09-621-976-1416

Query Match      72.2%; Score 16.6; DB 4; Length 404;
Best Local Similarity 82.6%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGCAGCAGGG 23
Db 389 GAAGGCCATGTAGAGCAACAGGG 367

RESULT 12
US-09-621-976-15579/c
; Sequence 15579, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15579
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (251)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (273)
; OTHER INFORMATION: a, c, g, t, unknown or other
US-09-621-976-15579

Query Match      72.2%; Score 16.6; DB 4; Length 446;
Best Local Similarity 82.6%; Pred. No. 91;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAGCAGCAGGG 23
Db 389 GAAGGCCATGTAGAGCAACAGGG 367

RESULT 13
US-09-621-976-181/c
; Sequence 181, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 67..390
; NAME/KEY: sig_peptide
; LOCATION: 67..126
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 8.39999961853027
; OTHER INFORMATION: seq AVVGCLLVPPAER/NK
US-09-621-976-181/c

```

US-09-107-532A-2051

Query Match 72.2%; Score 16.6; DB 4; Length 1416;
Best Local Similarity 82.6%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAAGCAGCAGG 23
Db 836 GAAATCCAGGAAAGCAGAGAG 858

RESULT 15
US-09-673-395A-3/c
; Sequence 3, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1571
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-3

Query Match 72.2%; Score 16.6; DB 4; Length 1571;
Best Local Similarity 82.6%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAAGCAGCAGG 23
Db 433 GAAGGCCATGTAGAGCAACAGG 411

Search completed: December 5, 2004, 07:17:53
Job time : 4.864 secs

LENGTH: 542
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 309..542
NAME/KEY: sig_peptide
LOCATION: 309..455
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.09999990463257
OTHER INFORMATION: seq LLYMAFLMLGGPS/DP
US-09-621-976-181

Query Match 72.2%; Score 16.6; DB 4; Length 542;
Best Local Similarity 82.6%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAATCCATGTAAAGCAGCAGG 23
Db 434 GAAGGCCATGTAGAGCAACAGG 412

RESULT 14
US-09-107-532A-2051
; Sequence 2051, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2051:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1416
; SEQUENCE DESCRIPTION: SEQ ID NO: 2051:

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ALIGNMENTS

```

US-10-027-880-5
; Sequence 5, Application US/10027880
; Publication No. US20030106105A1
; GENERAL INFORMATION:
; APPLICANT: HOFFMAN, BEATE
; TITLE OF INVENTION: PROMOTER EXPRESSED SPECIFICALLY
; TITLE OF INVENTION: VECTORS AND RECOMBINANT HOST CELLS
; TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANT
; TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANT
; FILE REFERENCE: CHRP:003US
; CURRENT APPLICATION NUMBER: US/10/027,880
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/FR00/01768
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7599
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-10-027-880-5

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	Query Match	Best Local Similarity	Score	DB 15	Length	DB 15	Length	DB 15	Length
Matches	192	Conservative	1	Mismatches	0	Indels	0	Gaps	0
QY	1	CTACGGCAATGTPACCGCTGATATTAATCAGTTATTCTGAAATATTTCTGAAATTTTAAACTTGC	60						
Db	6579	CTACGGCAATGTPACCGCTGATATTAATCAGTTATTCTGAAATATTTCTGAAATTTTAAACTTGC	6638						
QY	61	ATCAATAAAAWTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATTATCAATAAA	120						
Db	6639	ATCAATAAAATTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATTATCAATAAA	6698						

SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
1	192.6	46.3	7599	15	US-10-027-880-5	Sequence 5, Appli
2	190	45.7	6539	9	US-09-509-945-5	Sequence 5, Appli
3	190	45.7	6548	9	US-09-509-945-4	Sequence 4, Appli
C 4	189.6	45.6	4832	9	US-09-733-151-2	Sequence 2, Appli
C 5	189.6	45.6	4832	15	US-10-375-333-2	Sequence 2, Appli
C 6	189.6	45.6	4946	9	US-09-733-151-1	Sequence 1, Appli
C 7	189.6	45.6	4946	15	US-10-375-333-1	Sequence 1, Appli
C 8	189.6	45.6	5349	9	US-09-970-521-7	Sequence 7, Appli
C 9	179	43.0	1077	9	US-09-733-151-24	Sequence 24, Appli
C 10	179	43.0	1077	15	US-10-375-333-24	Sequence 24, Appli
C 11	154.6	37.2	4465	13	US-10-047-543-13	Sequence 13, Appli
C 12	154.6	37.2	6602	13	US-10-047-543-100	Sequence 100, Appli

121 TATTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATGCTTTTCTTATC 180
6699 TATTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATGCTTTTCTTATC 6758
181 GACCATGTACATC 193
6759 GACCATGTACATC 6771

RESULT 2
US-09-509-945-5
; Sequence 5, Application US/09509945
; Patent No. US20020166140A1
; GENERAL INFORMATION:
; APPLICANT: HAMADA, Kazuyuki et al.
; TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
; FILE REFERENCE: 0230-0148P
; CURRENT APPLICATION NUMBER: US/09/509,945
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 6539
; TYPE: DNA
; ORGANISM: Escherichia coli LE392
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone: pTS431
US-09-509-945-5

Query Match 45.7%; Score 190; DB 9; Length 6539;
Best Local Similarity 99.0%; Pred. No. 3.6e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACCACTGATATATATCAGTTATTGAAATATTCTGAAATTTAACTTGC 60
DB 6342 CTACGGCAATGTACCACTGATATATATCAGTTATTGAAATATTCTGAAATTTAACTTGC 6401

QY 61 ATCAATAAAATTTATGTTTTGCTTGGACTATATAATCACTGACTTGTATTATCAATAAA 120
DB 6402 ATCAATAAAATTTATGTTTTGCTTGGACTATATAATCACTGACTTGTATTATCAATAAA 6461

QY 121 TATTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATGCTTTTCTTATC 180
DB 6462 TATTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATGCTTTTCTTATC 6521

QY 181 GACCATGTACAT 192
DB 6522 GACCATGTACGT 6533

RESULT 3
US-09-509-945-4
; Sequence 4, Application US/09509945
; Patent No. US20020166140A1
; GENERAL INFORMATION:
; APPLICANT: HAMADA, Kazuyuki et al.
; TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
; FILE REFERENCE: 0230-0148P
; CURRENT APPLICATION NUMBER: US/09/509,945
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Escherichia coli LE392
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Clone: pTS172
US-09-509-945-4

Query Match 45.7%; Score 190; DB 9; Length 6548;
Best Local Similarity 99.0%; Pred. No. 3.6e-29;
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACCACTGATATATATCAGTTATTGAAATATTCTGAAATTTAACTTGC 60
DB 6351 CTACGGCAATGTACCACTGATATATATCAGTTATTGAAATATTCTGAAATTTAACTTGC 6410

QY 61 ATCAATAAAATTTATGTTTTGCTTGGACTATATAATCACTGACTTGTATTATCAATAAA 120
DB 6411 ATCAATAAAATTTATGTTTTGCTTGGACTATATAATCACTGACTTGTATTATCAATAAA 6470

QY 121 TATTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATGCTTTTCTTATC 180
DB 6471 TATTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATGCTTTTCTTATC 6530

QY 181 GACCATGTACAT 192
DB 6531 GACCATGTACGT 6542

RESULT 4
US-09-733-151-2/c
; Sequence 2, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 4832
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4832)
; OTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2

Query Match 45.6%; Score 189.6; DB 9; Length 4832;
Best Local Similarity 99.5%; Pred. No. 3.9e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACCACTGATATATATCAGTTATTGAAATATTCTGAAATTTAACTTGC 60
DB 243 CTACGGCAATGTACCACTGATATATATCAGTTATTGAAATATTCTGAAATTTAACTTGC 184

QY 61 ATCAATAAAATTTATGTTTTGCTTGGACTATATAATCACTGACTTGTATTATCAATAAA 120
DB 183 ATCAATAAAATTTATGTTTTGCTTGGACTATATAATCACTGACTTGTATTATCAATAAA 124

QY 121 TATTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATGCTTTTCTTATC 180
DB 123 TATTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATGCTTTTCTTATC 64

QY 181 GACCATGTAC 190
DB 63 GACCATGTAC 54

RESULT 5
US-10-375-332-2/c
; Sequence 2, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME

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; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 4832
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4832)
; OTHER INFORMATION: Plasmid pTHW118
US-10-375-332-2

Query Match 45.6%; Score 189.6; DB 15; Length 4832;
Best Local Similarity 99.5%; Pred. No. 4e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACACGCTGATATAATCAGTTATTGAAATATTTCTGAAATTTAAACTTGC 60
DB 243 CTACGGCAATGTACACGCTGATATAATCAGTTATTGAAATATTTCTGAAATTTAAACTTGC 184
QY 61 ATCAATAAATTTATGTTTTCCTTGGACTATAATACCTGACTTGTATTTTATCAATAAA 120
DB 183 ATCAATAAATTTATGTTTTCCTTGGACTATAATACCTGACTTGTATTTTATCAATAAA 124
QY 121 TATTTAACTATATTTCTTCAAGATGGGAATTAACATCTACAAATTCCTTTTCTTATC 180
DB 123 TATTTAACTATATTTCTTCAAGATGGGAATTAACATCTACAAATTCCTTTTCTTATC 64
QY 181 GACCATGTAC 190
DB 63 GACCATGTAC 54

; RESULT 7
US-10-375-332-1/c
; Sequence 1, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 4946
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4946)
; OTHER INFORMATION: Plasmid pTHW107
US-10-375-332-1

Query Match 45.6%; Score 189.6; DB 15; Length 4946;
Best Local Similarity 99.5%; Pred. No. 4e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACACGCTGATATAATCAGTTATTGAAATATTTCTGAAATTTAAACTTGC 60
DB 243 CTACGGCAATGTACACGCTGATATAATCAGTTATTGAAATATTTCTGAAATTTAAACTTGC 184
QY 61 ATCAATAAATTTATGTTTTCCTTGGACTATAATACCTGACTTGTATTTTATCAATAAA 120
DB 183 ATCAATAAATTTATGTTTTCCTTGGACTATAATACCTGACTTGTATTTTATCAATAAA 124
QY 121 TATTTAACTATATTTCTTCAAGATGGGAATTAACATCTACAAATTCCTTTTCTTATC 180
DB 123 TATTTAACTATATTTCTTCAAGATGGGAATTAACATCTACAAATTCCTTTTCTTATC 64
QY 181 GACCATGTAC 190
DB 63 GACCATGTAC 54

; RESULT 8
US-09-970-921-7/c
; Sequence 7, Application US/09970921
; Patent No. US20020133845A1
; GENERAL INFORMATION:
; APPLICANT: Frank Michiels et al.
; TITLE OF INVENTION: Improved Barstar Gene
; FILE REFERENCE: 2428-0108P
; CURRENT APPLICATION NUMBER: US/09/970,921
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 5349
```

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; NAME/KEY: acid, "T-DNA of pTTS243"
; LOCATION: (1)..(25)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
; LOCATION: Complement(1)..(25)
; NAME/KEY: label = RB, "T-DNA right border"
; NAME/KEY: misc feature
; LOCATION: Complement(198)..(331)
; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
; NAME/KEY: misc feature
; LOCATION: Complement(332)..(883)
; OTHER INFORMATION: label = bar, "region coding for phosphinotricin
; OTHER INFORMATION: acetyl transferase"
; NAME/KEY: misc feature
; LOCATION: Complement(884)..(2258)
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: Virus"
; NAME/KEY: misc feature
; LOCATION: (2281)..(3969)
; OTHER INFORMATION: label = pPi, "promoter of E1 gene of rice (WO
; OTHER INFORMATION: 92/13956)"
; NAME/KEY: misc feature
; LOCATION: (3970)..(4245)
; OTHER INFORMATION: label = synb*, "improved barstar DNA"
; NAME/KEY: misc feature
; LOCATION: (4246)..(4577)
; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
; OTHER INFORMATION: end of chalcone synthase gene"
; NAME/KEY: misc feature
; LOCATION: Complement(5325)..(5349)
; OTHER INFORMATION: label = LB, "T-DNA left border"
;
US-09-970-921-7
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Query Match 45.6%; Score 189.6; DB 9; Length 5349;
Best Local Similarity 99.5%; Pred. No. 4.1e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACCAAGCTGATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 60
Db 243 CTACGGCAATGTACCAAGCTGATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 184

QY 61 ATCAATAAAATTTATGTTTTGCTTGGACTATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 120
Db 183 ATCAATAAAATTTATGTTTTGCTTGGACTATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 124

QY 121 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 180
Db 123 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 64

QY 181 GACCATGTAC 190
Db 63 GACCATGTAC 54
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RESULT 9
US-09-733-151-24/c
; Sequence 24, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
; LENGTH: 1077
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; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1077)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
;
US-09-733-151-24

Query Match 43.0%; Score 179; DB 9; Length 1077;
Best Local Similarity 98.9%; Pred. No. 3.7e-27;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACCAAGCTGATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 60
Db 1060 CTACGGCAATGTACCAAGCTGATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 1001

QY 61 ATCAATAAAATTTATGTTTTGCTTGGACTATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 120
Db 1000 ATCAATAAAATTTATGTTTTGCTTGGACTATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 941

QY 121 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 180
Db 940 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 881

QY 181 G 181
Db 880 G 880
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RESULT 10
US-10-375-332-24/c
; Sequence 24, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1077)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
;
US-10-375-332-24
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Query Match 43.0%; Score 179; DB 15; Length 1077;
Best Local Similarity 98.9%; Pred. No. 3.7e-27;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACCAAGCTGATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 60
Db 1060 CTACGGCAATGTACCAAGCTGATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 1001

QY 61 ATCAATAAAATTTATGTTTTGCTTGGACTATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 120
Db 1000 ATCAATAAAATTTATGTTTTGCTTGGACTATATATCAGTTATTGAAATATTTCTGAATTTAACTTGC 941

QY 121 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 180
Db 940 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 881

QY 181 G 181
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Db 880 G 880

RESULT 11

US-10-047-542-13

Sequence 13, Application US/10047542

Publication No. US20020168367A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W.

APPLICANT: WYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905.0004.CIP1

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR FILING DATE: 2001-04-28

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 4465

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: Expression-type plasmid pBMSF-1

FEATURE:

NAME/KEY: modified_base

LOCATION: (2150)

OTHER INFORMATION: a, c, t or g

FEATURE:

NAME/KEY: modified_base

LOCATION: (2214)..(2215)

OTHER INFORMATION: a, c, t or g

US-10-047-542-13

Query Match 37.2%; Score 154.6; DB 13; Length 4465;

Best Local Similarity 99.4%; Pred. No. 5.9e-22;

Matches 154; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTACGGCAATGTACAGCTGATATAATCAGTTATTGAAATATTCTGAAATTTAAACTTGC 60

Db 3579 CTACGGCAATGTACAGCTGATATAATCAGTTATTGAAATATTCTGAAATTTAAACTTGC 3638

Qy 61 ATCAATAAAATTTATGTTTTCTTGGACTATAATACCTGACTTCTTATTTATCAATAAA 120

Db 3639 ATCAATAAAATTTATGTTTTCTTGGACTATAATACCTGACTTCTTATTTATCAATAAA 3698

Qy 121 TATTTAACTATATTCTTTTCAAGATGGGAATTAA 155

Db 3699 TATTTAACTATATTCTTTTCAAGATGGGAATTAA 3733

RESULT 12

US-10-047-542-100

Sequence 100, Application US/10047542

Publication No. US20020168367A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W.

APPLICANT: WYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905.0004.CIP1

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR FILING DATE: 2001-04-28

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 100

LENGTH: 6602

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism:

OTHER INFORMATION: PGFTV-hpt-ocs-358J/SC

US-10-047-542-101

Query Match 37.2%; Score 154.6; DB 13; Length 7129;

Best Local Similarity 99.4%; Pred. No. 6.9e-22;

Matches 154; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTACGGCAATGTACAGCTGATATAATCAGTTATTGAAATATTCTGAAATTTAAACTTGC 60

Db 887 CTACGGCAATGTACAGCTGATATAATCAGTTATTGAAATATTCTGAAATTTAAACTTGC 828

Qy 61 ATCAATAAAATTTATGTTTTCTTGGACTATAATACCTGACTTCTTATTTATCAATAAA 120

Db 827 ATCAATAAAATTTATGTTTTCTTGGACTATAATACCTGACTTCTTATTTATCAATAAA 768

Qy 121 TATTTAACTATATTCTTTTCAAGATGGGAATTAA 155

Db 767 TATTTAACTATATTCTTTTCAAGATGGGAATTAA 733

RESULT 14

US-10-047-542-14/c

Sequence 14, Application US/10047542

Publication No. US20020168367A1
GENERAL INFORMATION: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: 60/200,298
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 8074
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Expression-type plasmid pEMSP-1spJSC
FEATURE:
NAME/KEY: modified_base
LOCATION: (2315)
OTHER INFORMATION: a, c, t or g
US-10-047-542-14

Query Match 37.2%; Score 154.6; DB 13; Length 8074;
Best Local Similarity 99.4%; Pred. No. 7.2e-22;
Matches 154; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTACGGCAATGACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAACTTGC 60
DB 887 CTACGGCAATGACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAACTTGC 828
QY 61 ATCAATAAAWTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATCAATAAA 120
DB 827 ATCAATAAAWTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATCAATAAA 768
QY 121 TATTAACTATATTTCTTCAAGATGGGAATTA 155
DB 767 TATTAACTATATTTCTTCAAGATGGGAATTA 733

RESULT 15
US-09-847-057-4/c
Sequence 4, Application US/09847057
Patent No. US2002000493A1
GENERAL INFORMATION:
APPLICANT: AGRINOMICS, LLC.
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLAN
FILE REFERENCE: PAGODA
CURRENT APPLICATION NUMBER: US/09/847,057
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 8340
TYPE: DNA
ORGANISM: Binary vector pAGI4002
US-09-847-057-4

Query Match 37.2%; Score 154.6; DB 9; Length 8340;
Best Local Similarity 99.4%; Pred. No. 7.2e-22;
Matches 154; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTACGGCAATGACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAACTTGC 60
DB 6648 CTACGGCAATGACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAACTTGC 6589
QY 61 ATCAATAAAWTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATCAATAAA 120

Db 6588 ATCAATAAAWTTATGTTTTTGGCTGGACTATAATACCTGACTTGTATTATCAATAAA 6529
QY 121 TATTAACTATATTTCTTCAAGATGGGAATTA 155
DB 6528 TATTAACTATATTTCTTCAAGATGGGAATTA 6494

Search completed: December 5, 2004, 09:36:22
Job time : 331.898 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	415.6	99.9	416	4	US-09-430-497A-10		Sequence 10, Appl
2	380.8	91.5	415	4	US-09-430-497A-8		Sequence 8, Appl
3	192.6	46.3	5864	3	US-08-894-440-4		Sequence 4, Appl
4	192.6	46.3	5864	3	US-09-458-093-4		Sequence 4, Appl
5	192.6	46.3	5865	4	US-09-430-497A-1		Sequence 1, Appl
6	190	45.7	6548	3	US-08-894-440-1		Sequence 1, Appl
7	190	45.7	6548	3	US-08-817-188-2		Sequence 2, Appl
8	190	45.7	6548	3	US-09-458-093-1		Sequence 1, Appl
9	190	45.7	7811	2	US-08-894-440-5		Sequence 5, Appl
10	189.6	45.6	1303	3	US-08-894-440-2		Sequence 2, Appl
11	189.6	45.6	1303	3	US-09-458-093-2		Sequence 2, Appl
12	189.6	45.6	3200	1	US-08-453-104-23		Sequence 23, Appl
13	189.6	45.6	3200	2	US-08-694-824-23		Sequence 23, Appl
14	189.6	45.6	4832	4	US-09-457-037B-2		Sequence 2, Appl
15	189.6	45.6	4832	4	US-09-733-151-2		Sequence 2, Appl
16	189.6	45.6	4946	3	US-08-817-188-1		Sequence 1, Appl
17	189.6	45.6	4946	4	US-09-457-037B-1		Sequence 1, Appl
18	189.6	45.6	4946	4	US-09-733-151-1		Sequence 1, Appl
19	189.6	45.6	5349	3	US-09-068-101-7		Sequence 7, Appl
20	189.6	45.6	5349	4	US-09-970-921-7		Sequence 7, Appl
21	189.6	45.6	5560	3	US-08-817-188-5		Sequence 5, Appl
22	189.6	45.6	5865	4	US-09-430-497A-1		Sequence 1, Appl
23	189.6	45.6	7566	2	US-08-233-016-23		Sequence 23, Appl
24	189.6	45.6	7639	2	US-08-232-016-22		Sequence 22, Appl
25	188	45.2	5864	3	US-08-894-440-4		Sequence 4, Appl
26	188	45.2	5864	3	US-09-458-093-4		Sequence 4, Appl
27	179	43.0	1077	4	US-09-457-037B-24		Sequence 24, Appl

Db 241 CCTGCTGCTTTACATGGATTTCTCGCTACTATTGTATAGTGTATATACCGTATA 300
QY 301 ATGTACATATATTATATGAACATGATTAACTGTTGAGTTGTTCTCATCGTAAGAGT 360
Db 301 ATGTACATATATTATATGAACATGATTAACTGTTGAGTTGTTCTCATCGTAAGAGT 360
QY 361 TTCAATATGTAATGTTGAAGATCAAAACCCAAAATCATGAACACCAAACTCGAT 416
Db 361 TTCAATATGTAATGTTGAAGATCAAAACCCAAAATCATGAACACCAAACTCGAT 416

RESULT 2

US-09-430-497A-8/c
; Sequence 8, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; FILE REFERENCE: SAME
; CURRENT APPLICATION NUMBER: US/09/430,497A
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5' border
; OTHER INFORMATION: flanking region of elite event MS-B2
; NAME/KEY: misc feature
; LOCATION: (1)..(234)
; OTHER INFORMATION: plant DNA
; NAME/KEY: misc feature
; LOCATION: (235)..(415)
; OTHER INFORMATION: T-DNA
US-09-430-497A-8

Query Match 91.5%; Score 380.8; DB 4; Length 415;
Best Local Similarity 98.5%; Pred. No. 6.7e-85;
Matches 404; Conservative 1; Mismatches 3; Indels 2; Gaps 2;
QY 1 CTACGGCAATGTACCACTGATATATCAATCAGTATTGAAATATTTCTGAATTTAAACTTGC 60
Db 415 CTACGGCAATGTACCACTGATATATCAATCAGTATTGAAATATTTCTGAATTTAAACTTGC 356
QY 61 ATCAATAAATTAATGTTTCTGCTGGACTATAAATCACTGACTTCTTATTTATCAATAAA 120
Db 355 ATCAATAAATTAATGTTTCTGCTGGACTATAAATCACTGACTTCTTATTTATCAATAAA 296
QY 121 TATTTAACATATATTTCTTCAAGATGGATTAACATCTACAAATTCCTTTCTTATC 180
Db 295 TATTTAACATATATTTCTTCAAGATGGATTAACATCTACAAATTCCTTTCTTATC 236
QY 181 GACCATGPACATCTACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 239
Db 235 GGCCATGTACATCTACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 176
QY 240 CCCCTGCTGCTTACATGGATTTCTCGCTACTATTTGTATAGTGTATATATACCGTAT 299
Db 175 CCCCTGCTGCTTACATGGATTTCTCGCTACTATTTGTATAGTGTATATATACCGTAT 117
QY 300 AATGTACATATATTATATGAACATGATTAACTGTTGAGTTGTTCTCATCCGTAAGAG 359
Db 116 AATGTACATATATTATATGAACATGATTAACTGTTGAGTTGTTCTCATCCGTAAGAG 57
QY 360 TTTCAATATGTAATGTTGAAGATCAAAACCCAAAATCATGAACACCAAA 409
Db 56 TTTCAATATGTAATGTTGAAGATCAAAACCCAAAATCATGAACACCAAA 7

RESULT 3
US-08-894-440-4
; Sequence 4, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5864
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pTCO113
; NAME/KEY: misc feature
; LOCATION: Complement(1)..(25)
; OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement(98)..(330)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement(331)..(882)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement(883)..(2608)
; OTHER INFORMATION: promoter of small subunit gene of Rubisco of
; OTHER INFORMATION: Arabidopsis (Pssu)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2659)..(3031))
; OTHER INFORMATION: region containing polyadenylation signal of
; OTHER INFORMATION: napaline synthase gene of Agrobacterium T-DNA
; OTHER INFORMATION: (3'nos)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((3032)..(3367))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((3368)..(4877))
; OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
; OTHER INFORMATION: tabacum (PTA29)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4924)..(5216)
; OTHER INFORMATION: promoter of napaline synthase gene of
; OTHER INFORMATION: Agrobacterium T-DNA (Phos)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5217)..(5489)
; OTHER INFORMATION: region coding for barstar of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5490)..(5765)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((5840)..(5864))

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/ OTHER INFORMATION: left border of Agrobacterium T-DNA
US-08-894-440-4
Query Match          46.3%; Score 192.6; DB 3; Length 5864;
Best Local Similarity 99.5%; Pred. No. 2.2e-38;
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAAATTTAAACTTGC 60
Db 5620 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAAATTTAAACTTGC 5679

QY 61 ATCAATAAAATTTATGTTTCTGGACTATAATACCTGACTTCTTATTTATCAATAAA 120
Db 5680 ATCAATAAAATTTATGTTTCTGGACTATAATACCTGACTTCTTATTTATCAATAAA 5739

QY 121 TATTTAACTATATTTCTTCAAGATGGAATTAACATCTACAAATTCCTTTTCTTATC 180
Db 5740 TATTTAACTATATTTCTTCAAGATGGAATTAACATCTACAAATTCCTTTTCTTATC 5799

QY 181 GACCATGTACATC 193
Db 5800 GACCATGTACATC 5812

RESULT 4
US-09-458-093-4
/ Sequence 4; Application US/09458093
/ Patent No. 634602
/ GENERAL INFORMATION:
/ APPLICANT: PLANT GENETIC SYSTEMS N.V.
/ TITLE OF INVENTION: Method to obtain male sterile plants
/ FILE REFERENCE: NMSCOR
/ CURRENT APPLICATION NUMBER: US/09/458,093
/ CURRENT FILING DATE: 1999-12-10
/ PRIOR APPLICATION NUMBER: 08/894,440
/ PRIOR FILING DATE: 1997-11-12
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ TYPE: DNA
/ LENGTH: 5864
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
/ OTHER INFORMATION: plasmid pTC0113
/ NAME/KEY: misc feature
/ LOCATION: Complement((1)..(25))
/ OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
/ NAME/KEY: misc feature
/ LOCATION: Complement((98)..(330))
/ OTHER INFORMATION: region containing polyadenylation signal of gene 7
/ OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
/ NAME/KEY: misc feature
/ LOCATION: Complement((331)..(882))
/ OTHER INFORMATION: region coding for phosphinothricin acetyl
/ OTHER INFORMATION: transferase (bar)
/ NAME/KEY: misc feature
/ LOCATION: Complement((883)..(2508))
/ OTHER INFORMATION: promoter of small subunit gene of Rubisco of
/ OTHER INFORMATION: Arabidopsis (Pssu)
/ NAME/KEY: misc feature
/ LOCATION: Complement((2659)..(3031))
/ OTHER INFORMATION: region containing polyadenylation signal of
/ OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
/ OTHER INFORMATION: (3'nos)
/ NAME/KEY: misc feature
/ LOCATION: Complement((3032)..(3367))
/ OTHER INFORMATION: region coding for barnase of Bacillus
/ OTHER INFORMATION: amyloliquefaciens
/ NAME/KEY: misc feature
/ LOCATION: Complement((3368)..(4877))
/ OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
/ OTHER INFORMATION: tabacum (PTA29)
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Qy	121	TAATTTAAACTATATTTCTTTCAAGATGGGAATTAA	CACTACAAATGGCTTTTCTTTATC	180
Db	5741	TAATTTAAACTATATTTCTTTCAAGATGGGAATTAA	CACTACAAATGGCTTTTCTTTATC	5800
Qy	181	GACCATGTACATC	193	
Db	5801	GACCATGTACATC	5813	

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RESULT 6
US-08-894-440-1
; Sequence 1, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pFS174
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2003)
; OTHER INFORMATION: of pUC19 derived vector sequences (vector)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2019)..(2283))
; OTHER INFORMATION: 3' nos: region containing polyadenylation signal
; OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2284)..(2624))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: promoter of the stamen-specific E1 gene of rice
; OTHER INFORMATION: (pE1)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4336)..(5710)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5711)..(6262)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: region containing polyadenylation signal fo gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
US-08-894-440-1

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Qy	121	TATTTAAACATATATTTCTTTCAAGATGGGAATAAACATCTACAAATGGCTTTTCTTATC	180
Db	6471	TATTTAAACATATATTTCTTTCAAGATGGGAATTAACATCTACAAATGGCTTTTCTTATC	
Qy	181	GACCATGTACAT	192
Db	6531	GACCATGTACGT	6542

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RESULT 7
US-08-817-188-2
; Sequence 2, Application US/08817188
; Patent No. 6074876
; GENERAL INFORMATION:
; APPLICANT: DE BLOCK, MARC
; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
; FILE REFERENCE: 2121-0127P
; CURRENT APPLICATION NUMBER: US/08/817,188
; CURRENT FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: PCT/EP96/03366
; EARLIER FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: EP 95401844.6
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid PTS172
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2019)..(2288))
; OTHER INFORMATION: 3' nos: 3' untranslated region containing the
; OTHER INFORMATION: polyadenylation signal of the nopaline synthase
; OTHER INFORMATION: gene of Agrobacterium T-DNA.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2289)..(2624))
; OTHER INFORMATION: barnase: region coding for barnase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: Pfl: promoter region of El gene of rice
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4336)..(5170)
; OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
; OTHER INFORMATION: Virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((5711)..(6262))
; OTHER INFORMATION: bar: region coding for phosphinotricin
; OTHER INFORMATION: acetyltransferase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6283)..(6496)
; OTHER INFORMATION: 3'g7: 3' untranslated region containing the
; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
; OTHER INFORMATION: T-DNA
US-08-817-188-2

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	6411	121	6471	181	6531
Db	:				
Qy	ATCAATAAATTATGTTTTGCTGGACTATAACCTGACTTGTATTATTTATCAATAAA	TATTTAAACATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTCTTATC	TATTTAAACATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTCTTATC	GACCATCATACAT	GACCATGTACGT
Db					
Qy					
Db					

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RESULT 8
US-09-458-093-1
; Sequence 1, Application US/09458093
; Patent No. 6344602
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NM5C0F
; CURRENT APPLICATION NUMBER: US/09/458,093
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 08/894,440
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Description of Artificial Sequence: plasmid pTS174
; LOCATION: (1)..(2003)
; OTHER INFORMATION: pUC19 derived vector sequences (vector)
; NAME/KEY: misc_feature
; LOCATION: (1)..(2003)
; NAME/KEY: misc_feature
; LOCATION: Complement((2019)..(2283))
; OTHER INFORMATION: 3' nos: region containing polyadenylation signal
; OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
; NAME/KEY: misc_feature
; LOCATION: Complement((2284)..(2624))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; NAME/KEY: misc_feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: promoter of the stamen-specific E1 gene of rice
; OTHER INFORMATION: (pel)
; NAME/KEY: misc_feature
; LOCATION: (4336)..(5710)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
; NAME/KEY: misc_feature
; LOCATION: (5711)..(6262)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; NAME/KEY: misc_feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: region containing polyadenylation signal fo gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
US-09-458-093-1

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Db      6471  TATTTAACTATATTTCTTTCAAGATGGGAATTAAACATCTACAAATGCCTTTCCTTATC 6530
QY      181  GACCATGTACAT 192
Db      6531  GACCATGTACGT 6542

RESULT 9
US-08-549-680A-5/c
; Sequence 5, Application US/08549680A
; Patent No. 5962768
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, MARCUS
; APPLICANT: REYNAERTS, ARLETTE
; APPLICANT: GOSSELE, VERONIQUE
; APPLICANT: VAN AARSEN, ROEL
; TITLE OF INVENTION: MARKER GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,680A
; FILING DATE: 16 JANUARY 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-0111P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7811 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (synthetic)
; FEATURE:
; NAME/KEY: misc recomb
; LOCATION: 1..7811
; OTHER INFORMATION: /label= vector pTRVA3
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 194..218
; OTHER INFORMATION: /note= "T-DNA right border"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 484..684
; OTHER INFORMATION: /note= "the 3' end formation and
; OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (729..1340)
; OTHER INFORMATION: /note= "the aac(6') coding
; OTHER INFORMATION: sequence"
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 1341..1756
; OTHER INFORMATION: /label= 35S promoter
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: 3001..3023
; OTHER INFORMATION: /note="T-DNA left border
; OTHER INFORMATION: sequences"
US-08-549-680A-5

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Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTACGGCAATGTACCAAGCTGATATAATCAGTTATTGAAATATTTCTGAAATTTAACTTGC 60
Db 629 CTACGGCAATGTACCAAGCTGATATAATCAGTTATTGAAATATTTCTGAAATTTAACTTGC 570

QY 61 ATCAATAAAWTTATGTTTTTGTGGACTATATAATACCTGACTTGTATTATTTATCAATAAA 120
Db 569 ATCAATAAAWTTATGTTTTTGTGGACTATATAATACCTGACTTGTATTATTTATCAATAAA 510

QY 121 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 180
Db 509 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 450

QY 181 GACCATGTACAT 192
Db 449 GACCATGTACGT 438

RESULT 10
US-08-894-440-2
; Sequence 2, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1303
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HindIII-BcoRI
; OTHER INFORMATION: fragment of pTS88
; NAME/KEY: misc_feature
; LOCATION: (1)..(35)
; OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36)..(694)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain
; OTHER INFORMATION: CM1841 (P35S)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (695)..(967)
; OTHER INFORMATION: region coding for barstar of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (968)..(1287)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'/g7)
; NAME/KEY: (1288)..(1303)
; OTHER INFORMATION: polylinker of pGEM2
US-08-894-440-2

Query Match
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Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TATTTAACTATATTTCTTTCAAGATGGGAATTAACATCTACAATTCGCTTTTCTTATC 180
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Qy 181 GACCATGTAC 190
Db 1278 GACCATGTAC 1287
RESULT 12
US-08-453-104-23
; Sequence 23, Application US/08453104
; Patent No. 5633446
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; TITLE OF INVENTION: IN PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453.104
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
; US-08-453-104-23
Query Match 45.6%; Score 189.6; DB 1; Length 3200;
Best Local Similarity 99.5%; Pred. No. 1.1e-37;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3012 ATCAATAAATTTATGTTTGTGCTGACTATATAATACCTGACTTGTATTATTAATCAATAA 3071
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Db 3072 TATTTAAACATATATTTCTTCAAGATGGGATTAACATCTACAAATTCCTTTCTATC 3131
Qy 181 GACCATGTAC 190
Db 3132 GACCATGTAC 3141
RESULT 13
US-08-694-824-23
; Sequence 23, Application US/08694824
; Patent No. 5877306
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; TITLE OF INVENTION: IN PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,824
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
; US-08-694-824-23
Query Match 45.6%; Score 189.6; DB 2; Length 3200;
Best Local Similarity 99.5%; Pred. No. 1.1e-37;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTACGGCAATGACAGCTGATATATCACTTATTGAAATATTTCTGAATTTAAACTTGC 60
Db 2952 CTACGGCAATGACAGCTGATATATCACTTATTGAAATATTTCTGAATTTAAACTTGC 3011

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 05:20:20 ; Search time 69.72 Seconds
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Title: US-09-698-903B-8

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Searched: 824507 seqs, 35539441 residues

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Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	415	100.0	415	US-09-430-497A-8	Sequence 8, Appli
2	380.8	91.8	416	US-09-430-497A-10	Sequence 10, Appli
3	191.4	46.1	5864	US-08-894-440-4	Sequence 4, Appli
4	191.4	46.1	5864	US-09-458-093-4	Sequence 4, Appli
5	191.4	46.1	5865	US-09-430-497A-1	Sequence 1, Appli
6	188.8	45.5	6548	US-08-894-440-1	Sequence 1, Appli
7	188.8	45.5	6548	US-08-817-188-2	Sequence 2, Appli
8	188.8	45.5	6548	US-09-458-093-1	Sequence 1, Appli
9	188.8	45.5	7811	US-08-549-680A-5	Sequence 5, Appli
10	188.4	45.4	1303	US-08-894-440-2	Sequence 2, Appli
11	188.4	45.4	1303	US-09-458-093-2	Sequence 2, Appli
12	188.4	45.4	3200	US-08-453-104-23	Sequence 23, Appli
13	188.4	45.4	3200	US-08-694-824-23	Sequence 23, Appli
14	188.4	45.4	4832	US-09-457-037B-2	Sequence 2, Appli
15	188.4	45.4	4832	US-09-733-151-2	Sequence 2, Appli
16	188.4	45.4	4946	US-08-817-188-1	Sequence 1, Appli
17	188.4	45.4	4946	US-09-457-037B-1	Sequence 1, Appli
18	188.4	45.4	4946	US-09-733-151-1	Sequence 1, Appli
19	188.4	45.4	5349	US-09-068-101-7	Sequence 7, Appli
20	188.4	45.4	5349	US-09-970-921-7	Sequence 7, Appli
21	188.4	45.4	5560	US-08-817-188-5	Sequence 5, Appli
22	188.4	45.4	5560	US-09-430-497A-1	Sequence 1, Appli
23	188.4	45.4	7566	US-08-232-016-23	Sequence 23, Appli
24	188.4	45.4	7639	US-08-232-016-22	Sequence 22, Appli
25	186.8	45.0	5864	US-08-894-440-4	Sequence 4, Appli
26	186.8	45.0	5864	US-09-458-093-4	Sequence 4, Appli
27	179.4	43.2	1077	US-09-457-037B-24	Sequence 24, Appli

28	179.4	43.2	1077	4	US-09-733-151-24	Sequence 24, Appli
29	177	42.7	3201	1	US-08-453-104-22	Sequence 22, Appli
30	177	42.7	3201	2	US-08-694-824-22	Sequence 22, Appli
31	155	37.3	8340	4	US-09-847-057-4	Sequence 4, Appli
32	155	37.3	8340	4	US-09-874-926-4	Sequence 4, Appli
33	155	37.3	12241	4	US-09-948-138-4	Sequence 4, Appli
34	153	36.9	1186	1	US-08-064-121-2	Sequence 2, Appli
35	153	36.9	1186	1	US-08-478-015-2	Sequence 2, Appli
36	153	36.9	1186	3	US-08-475-975-2	Sequence 2, Appli
37	153	36.9	1186	3	US-09-084-889-2	Sequence 2, Appli
38	146	35.2	831	4	US-09-794-384A-7	Sequence 7, Appli
39	146	35.2	3153	3	US-09-080-625-3	Sequence 3, Appli
40	146	35.2	3153	3	US-09-695-782-3	Sequence 3, Appli
41	146	35.2	3336	3	US-09-080-625-2	Sequence 2, Appli
42	146	35.2	3336	4	US-09-695-782-2	Sequence 2, Appli
43	146	35.2	3694	3	US-09-080-625-5	Sequence 5, Appli
44	146	35.2	3694	4	US-09-695-782-5	Sequence 5, Appli
45	146	35.2	3877	3	US-09-080-625-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-430-497A-8
; Sequence 8, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BEUCKELBER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430,497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5' border
; OTHER INFORMATION: flanking region of elite event NS-B2
; NAME/KEY: misc feature
; LOCATION: (1)-(234)
; OTHER INFORMATION: plant DNA
; NAME/KEY: misc feature
; LOCATION: (235)-(415)
; OTHER INFORMATION: T-DNA
; OTHER INFORMATION: T-DNA
US-09-430-497A-8

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Best Local Similarity 100.0%; Pred. No. 4.2e-92;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TACGGATGAGAACCACTCAGCATTAATCATGTTTCATATAAATATATGTACATTATAC	120
Db	61	TACGGATGAGAACCACTCAGCATTAATCATGTTTCATATAAATATATGTACATTATAC	120
Qy	121	GTATATATACAGTATACAAATAGTAGCGAAGAAATCCATGTAAAGCAGAGGGGCACC	180
Db	121	GTATATATACAGTATACAAATAGTAGCGAAGAAATCCATGTAAAGCAGAGGGGCACC	180
Qy	181	ATCGTTTCAAGTATTAT	240
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Db 241 GAAAGGCAATTTGTAGATTAAATCCCATCTTGAAGAAATATAGTTTAAATATTAT 300
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Db 301 TGATAAAATACAGTCAGTATTATAGTCCCAAGCAAAACATAAATTTATTGATGCAAG 360
QY 361 TTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGCTGATCGCGTAG 415
Db 361 TTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGCTGATCGCGTAG 415

RESULT 2
US-09-430-497A-10/c
; Sequence 10, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BEUCKELSER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430,497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 3' border
; OTHER INFORMATION: flanking region of elite event MS-B2
; NAME/KEY: misc feature
; LOCATION: (1)..(193)
; OTHER INFORMATION: T-DNA
; NAME/KEY: misc feature
; LOCATION: (194)..(416)
; OTHER INFORMATION: plant DNA
US-09-430-497A-10

Query Match 91.8%; Score 380.8; DB 4; Length 416;
Best Local Similarity 98.5%; Pred No. 8.4e-84;
Matches 404; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

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QY 67 TCAGAACACTCACAGCATTAATCATGTTTCATATAATATATATATGATACATTAAC-GTATA 125
Db 349 TCAGAACACTCACAGCATTAATCATGTTTCATATAATATATATATGATACATTAACGTATA 290
QY 126 TATACAGGTATACAAATAGTAGCGAAGAAATCCATGTAAAGCAGAGGGGCGACCATGGT 185
Db 289 TATACAGGTATACAAATAGTAGCGAAGAAATCCATGTAAAGCAGAGGGGCGACCATGGT 230
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Db 229 TTC-AGTATTATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 171
QY 246 GGCAATTTGTAGATGTTAAATTCCTTCCATCTTGAAGAAATATAGTTTAAATATTATTGATA 305
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QY 306 AAATAACAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGATCAAGTTTAA 365
Db 110 AAATAACAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGATCAAGTTTAA 51
QY 366 ATTCAAGAATATTTCAATACTGATTATATATCAGCTGCTGATCGCGTAG 415
Db 50 ATTCAAGAATATTTCAATACTGATTATATATCAGCTGCTGATCGCGTAG 1

RESULT 3
US-08-894-440-4/c
; Sequence 4, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5864
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pTCO113
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((98)..(330))
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((331)..(882))
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((883)..(2608))
; OTHER INFORMATION: promoter of small subunit gene of Rubisco of
; OTHER INFORMATION: Arabidopsis (Pssu)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2659)..(3031))
; OTHER INFORMATION: region containing polyadenylation signal of
; OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
; OTHER INFORMATION: (3'nos)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((3032)..(3367))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((3368)..(4877))
; OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
; OTHER INFORMATION: tabacum (PTA29)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4924)..(5216)
; OTHER INFORMATION: promoter of nopaline synthase gene of
; OTHER INFORMATION: Agrobacterium T-DNA (Phos)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5217)..(5489)
; OTHER INFORMATION: region coding for barstar of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5490)..(5765)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((5840)..(5864))

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; OTHER INFORMATION: left border of Agrobacterium T-DNA
US-08-894-440-4

Query Match          46.1%; Score 191.4; DB 3; Length 5864;
Best Local Similarity 99.5%; Pred. No. 1.4e-37;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 223 GATGTACATGCCGATAGAAAGGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAA 282
DB 5812 GATGTACATGGTCGATAGAAAGGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAA 5753

QY 283 TATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAAACA 342
DB 5752 TATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAAACA 5693

QY 343 TAAATTTATGATGCAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGG 402
DB 5692 TAAATTTATGATGCAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGG 5633

QY 403 TACATTGCCGTAG 415
DB 5632 TACATTGCCGTAG 5620

RESULT 4
US-09-458-093-4/c
; Sequence 4, Application US/09458093
; Patent No. 6344602
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/09/458,093
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 08/894,440
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5864
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pTC0113
; NAME/KEY: misc feature
; LOCATION: Complement((1)..(25))
; OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
; NAME/KEY: misc feature
; LOCATION: Complement((98)..(330))
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; NAME/KEY: misc feature
; LOCATION: Complement((331)..(892))
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; NAME/KEY: misc feature
; LOCATION: Complement((883)..(2608))
; OTHER INFORMATION: promoter of small subunit gene of Rubisco of
; OTHER INFORMATION: Arabidopsis (Pssu)
; NAME/KEY: misc feature
; LOCATION: Complement((2659)..(3031))
; OTHER INFORMATION: region containing polyadenylation signal of
; OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
; OTHER INFORMATION: (3'nos)
; NAME/KEY: misc feature
; LOCATION: Complement((3032)..(3367))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; NAME/KEY: misc feature
; LOCATION: Complement((3368)..(4877))
; OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
; OTHER INFORMATION: tabacum (PTA29)
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; NAME/KEY: misc feature
; LOCATION: (4924)..(5216)
; OTHER INFORMATION: promoter of nopaline synthase gene of
; OTHER INFORMATION: Agrobacterium T-DNA (Phos)
; NAME/KEY: misc feature
; LOCATION: (5217)..(5489)
; OTHER INFORMATION: region coding for barstar of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; NAME/KEY: misc feature
; LOCATION: (5490)..(5765)
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; NAME/KEY: misc feature
; LOCATION: Complement((5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA
US-09-458-093-4

Query Match          46.1%; Score 191.4; DB 3; Length 5864;
Best Local Similarity 99.5%; Pred. No. 1.4e-37;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 223 GATGTACATGCCGATAGAAAGGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAA 282
DB 5812 GATGTACATGGTCGATAGAAAGGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAA 5753

QY 283 TATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAAACA 342
DB 5752 TATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAAACA 5693

QY 343 TAAATTTATGATGCAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGG 402
DB 5692 TAAATTTATGATGCAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGG 5633

QY 403 TACATTGCCGTAG 415
DB 5632 TACATTGCCGTAG 5620

RESULT 5
US-09-430-497A-1/c
; Sequence 1, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
; APPLICANT: WESTON, Brigitte
; APPLICANT: DE BEUCKELEER, Marc
; TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514412-2020
; CURRENT APPLICATION NUMBER: US/09/430,497A
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5865
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of
; OTHER INFORMATION: plasmid pCO113
US-09-430-497A-1

Query Match          46.1%; Score 191.4; DB 4; Length 5865;
Best Local Similarity 99.5%; Pred. No. 1.4e-37;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 223 GATGTACATGCCGATAGAAAGGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAA 282
DB 5813 GATGTACATGGTCGATAGAAAGGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAA 5754

QY 283 TATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAAACA 342
DB 5753 TATAGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAAACA 5694
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Db			
Qy	5693	403	5634
Db			

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RESULT 6
US-08-894-440-1/c
; Sequence 1, Application US/08894440
; Patent No. 6025546
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2003)
; OTHER INFORMATION: pUC19 derived vector sequences (vector)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: Complement((2019)..(2283))
; OTHER INFORMATION: 3' nos: region containing polyadenylation signal
; OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2284)..(2624))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: amyloliquefaciens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: promoter of the stamen-specific E1 gene of rice
; OTHER INFORMATION: [PE1]
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4336)..(5710)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5711)..(6262)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; OTHER INFORMATION: transferase (bar)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: region containing polyadenylation signal fo gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)

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QY	344	AAATTTATTGATGCAAGTTTAAATTCAGAAAATTTTCAATAACTGATTTATATCAGCTGGT	403
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QY	404	ACATTGCCGTAG	415
Db	6362	ACATTGCCGTAG	6351

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RESULT 7
US-08-817-188-2/c
; Sequence 2, Application US/08817188
; Patent No. 6074876
; GENERAL INFORMATION:
; APPLICANT: DE BLOCK, MARC
; TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR
; FILE REFERENCE: 2121-0127P
; CURRENT APPLICATION NUMBER: US/08/817,188
; CURRENT FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: PCT/EP96/03366
; EARLIER FILING DATE: 1996-07-31
; EARLIER APPLICATION NUMBER: EP 95401844.6
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pRS172
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2019)..(2288))
; OTHER INFORMATION: 3' nos: 3' untranslated region containing the
; OTHER INFORMATION: polyadenylation signal of the nopaline synthase
; OTHER INFORMATION: Gene of Agrobacterium T-DNA.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2289)..(2624))
; OTHER INFORMATION: barnase: region coding for barnase
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: PE1: promoter region of E1 gene of rice
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4316)..(5170)
; OTHER INFORMATION: B35S: 35S promoter region of Cauliflower Mosaic
; OTHER INFORMATION: Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: Complement((5711)..(6262))
; OTHER INFORMATION: bar: region coding for phosphinotricin
; OTHER INFORMATION: acetyltransferase
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: 3'g7: 3' untranslated region containing the
; OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium
; OTHER INFORMATION: T-DNA

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Db 6482 ATAGTTTAAATTTATTTGTAATAAATCAAGTCAGGTATTATAGTCCAGCAAAACAT 6423
Qy 344 AAATTTATGATGCAAGTTAAATTCAGAAATATTTCAATPACTGATTATATCAGCTGGT 403
Db 6422 AAATTTATGATGCAAGTTAAATTCAGAAATATTTCAATPACTGATTATATCAGCTGGT 6363
Qy 404 ACATTGCCGTAG 415
Db 6362 ACATTGCCGTAG 6351

RESULT 8
US-09-458-093-1/c
; Sequence 1, Application US/09458093
; Patent No. 6344602
; GENERAL INFORMATION:
; APPLICANT: PLANT GENETIC SYSTEMS N.V.
; TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/09/458,093
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 08/894,440
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
; NAME/KEY: misc feature
; LOCATION: (1)..(2003)
; OTHER INFORMATION: pUC19 derived vector sequences (vector)
; NAME/KEY: misc feature
; LOCATION: Complement((2019)..(2283))
; OTHER INFORMATION: 3' nos: region containing polyadenylation signal
; NAME/KEY: misc feature
; LOCATION: Complement((2284)..(2624))
; OTHER INFORMATION: region coding for barnase of Bacillus
; OTHER INFORMATION: anlyloquefaciens
; NAME/KEY: misc feature
; LOCATION: Complement((2625)..(4313))
; OTHER INFORMATION: promoter of the stamen-specific E1 gene of rice
; OTHER INFORMATION: (PE1)
; NAME/KEY: misc feature
; LOCATION: (4335)..(5710)
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
; NAME/KEY: misc feature
; LOCATION: (5711)..(6262)
; OTHER INFORMATION: region coding for phosphinothricin acetyl
; NAME/KEY: misc feature
; LOCATION: (6263)..(6496)
; OTHER INFORMATION: region containing polyadenylation signal fo gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
US-09-458-093-1

Query Match 45.5%; Score 188.8; DB 3; Length 6548;
Best Local Similarity 99.0%; Pred. No. 6.3e-37;
Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 224 ATGTACATGGCCGATAGAAAGCAATTTGTAGATGTTAATCCCATCTTTGAAAGAAAT 283
Db 6542 ACGTACATGGTCGATAGAAAGCAATTTGTAGATGTTAATCCCATCTTTGAAAGAAAT 6483
Qy 284 ATAGTTTAAATTTATTTGTAATAAATCAAGTCAGGTATTATAGTCCAGCAAAACAT 343
Db 6482 ATAGTTTAAATTTATTTGTAATAAATCAAGTCAGGTATTATAGTCCAGCAAAACAT 6423
Qy 344 AAATTTATGATGCAAGTTAAATTCAGAAATATTTCAATPACTGATTATATCAGCTGGT 403

Db 6422 AAATTTATGATGCAAGTTAAATTCAGAAATATTTCAATPACTGATTATATCAGCTGGT 6363
Qy 404 ACATTGCCGTAG 415
Db 6362 ACATTGCCGTAG 6351

RESULT 9
US-08-549-680A-5
; Sequence 5, Application US/08549680A
; Patent No. 5962768
; GENERAL INFORMATION:
; APPLICANT: CORNELIJSSEN, MARCUS
; APPLICANT: REYNAERTS, ARLETTE
; APPLICANT: GOSSELE, VERONIQUE
; APPLICANT: VAN BARSSEN, ROEL
; TITLE OF INVENTION: MARKER GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,680A
; FILING DATE: 16 JANUARY 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 2121-0111P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7811 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (synthetic)
; FEATURE:
; NAME/KEY: misc recomb
; LOCATION: 1..7811
; OTHER INFORMATION: /label= vector pTRVA3
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 194..218
; OTHER INFORMATION: /note= "T-DNA right border"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 484..684
; OTHER INFORMATION: /note= "the 3' end formation and
; OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: complement (729..1340)
; OTHER INFORMATION: /note= "the aac(6') coding
; OTHER INFORMATION: sequence"
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 1341..1756
; OTHER INFORMATION: /label= 35S promoter
; FEATURE:

Db 1167 ATTTATTCAGTCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 1108
QY 406 ATTGCGGTAG 415
Db 1107 ATTGCGGTAG 1098
RESULT 12
US-08-453-104-23/c
; Sequence 23, Application US/08453104
; Patent No. 5633446
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; TITLE OF INVENTION: IN PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 16-DEC-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
US-08-453-104-23
Query Match 45.4%; Score 188.4; DB 1; Length 3200;
Best Local Similarity 99.5%; Pred. No. 6.8e-37;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 226 GTACATGCCGATAGAAAGGCAATTTGTAGATGTTAAATTCATCTTGAAGAAATAT 285
Db 3141 GTACATGGTCGATAGAAAGGCAATTTGTAGATGTTAAATTCATCTTGAAGAAATAT 3082
QY 286 AGTTTAAATATTTATGATAAATAACAGTCAGGTATTATAGTCCAGCAAAAACATAA 345

Db 3081 AGTTTAAATATTTATGATAAATAACAGTCAGGTATTATAGTCCAGCAAAAACATAA 3022
QY 346 ATTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 405
Db 3021 ATTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 2962
QY 406 ATTGCGGTAG 415
Db 2961 ATTGCGGTAG 2952
RESULT 13
US-08-694-824-23/c
; Sequence 23, Application US/08694824
; Patent No. 5877306
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, Marc
; APPLICANT: SOETAERT, Piet
; APPLICANT: STAM, Maïke
; APPLICANT: DOCKX, Jan
; TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
; TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
; TITLE OF INVENTION: IN PLANT CELLS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: George Mason Bldg., Washington & Prince Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,824
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,869
; FILING DATE: 16-DEC-1992
; APPLICATION NUMBER: GB 90401055.0
; FILING DATE: 18-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa S
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 010830-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2078..2082
; OTHER INFORMATION: /note= "Nucleotides 2078-2082
; OTHER INFORMATION: wherein N is not known."
US-08-694-824-23
Query Match 45.4%; Score 188.4; DB 2; Length 3200;
Best Local Similarity 99.5%; Pred. No. 6.8e-37;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 226 GTACATGCCGATAGAAAGGCAATTTGTAGATGTTAAATTCATCTTGAAGAAATAT 285
Db 3141 GTACATGGTCGATAGAAAGGCAATTTGTAGATGTTAAATTCATCTTGAAGAAATAT 3082

QY 286 AGTTTAAATATTATTGATATAAATAACAAGTCAGGTATTATAGTCCAGCAAAACATAA 345
DB 3081 AGTTTAAATATTATTGATATAAATAACAAGTCAGGTATTATAGTCCAGCAAAACATAA 3022
QY 346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATPAACTGATTATATATCAGCTGGTAC 405
DB 3021 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATPAACTGATTATATATCAGCTGGTAC 2962
QY 406 ATTGCCGTAG 415
DB 2961 ATTGCCGTAG 2952

RESULT 14
US-09-457-037B-2
; Sequence 2, Application US/09457037B
; Patent No. 6506963
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/457,037B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4832
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4832)
; OTHER INFORMATION: T-DNA of Plasmid pTHW118
; NAME/KEY: misc feature
; LOCATION: (1883)..(4065)
; OTHER INFORMATION: Hpa I restriction fragment
US-09-457-037B-2

Query Match 45.4%; Score 188.4; DB 4; Length 4832;
Best Local Similarity 99.5%; Pred. No. 7.4e-37;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 226 GTACATGCCGATAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATAT 285
DB 54 GTACATGGTCGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATAT 113
QY 286 AGTTTAAATATTATTGATATAAATAACAAGTCAGGTATTATAGTCCAGCAAAACATAA 345
DB 114 AGTTTAAATATTATTGATATAAATAACAAGTCAGGTATTATAGTCCAGCAAAACATAA 173
QY 346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATPAACTGATTATATCAGCTGGTAC 405
DB 174 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATPAACTGATTATATCAGCTGGTAC 233
QY 406 ATTGCCGTAG 415
DB 234 ATTGCCGTAG 243

RESULT 15
US-09-733-151-2
; Sequence 2, Application US/09733151
; Patent No. 6583028
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037

; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 4832
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(4832)
; OTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2
Query Match 45.4%; Score 188.4; DB 4; Length 4832;
Best Local Similarity 99.5%; Pred. No. 7.4e-37;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 226 GTACATGCCGATAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATAT 285
DB 54 GTACATGGTCGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATAT 113
QY 286 AGTTTAAATATTATTGATATAAATAACAAGTCAGGTATTATAGTCCAGCAAAACATAA 345
DB 114 AGTTTAAATATTATTGATATAAATAACAAGTCAGGTATTATAGTCCAGCAAAACATAA 173
QY 346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATPAACTGATTATATCAGCTGGTAC 405
DB 174 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATPAACTGATTATATCAGCTGGTAC 233
QY 406 ATTGCCGTAG 415
DB 234 ATTGCCGTAG 243
Search completed: December 5, 2004, 07:17:52
Job time : 70.72 secs

Sequence 101, Appl
Sequence 14, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 4, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 24, Appl
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Sequence 28, Appl
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Sequence 3, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 101, Appl
Sequence 11, Appl
Sequence 8, Appl
Sequence 9, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 1192, Ap

13 155 37.3 7129 13 US-10-047-542-101
14 155 37.3 8074 13 US-10-047-542-14
15 155 37.3 8340 9 US-09-847-057-4
16 155 37.3 8340 9 US-09-874-926-4
17 155 37.3 12079 16 US-10-250-821-22
18 155 37.3 12079 16 US-10-250-553-22
19 155 37.3 12085 16 US-10-250-821-21
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21 155 37.3 12093 16 US-10-250-821-20
22 155 37.3 12093 16 US-10-250-553-20
C 23 155 37.3 12241 9 US-09-948-138-4
C 24 155 37.3 12241 13 US-10-033-190-5
C 25 155 37.3 12241 15 US-10-407-845A-4
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C 32 155 37.3 17752 16 US-10-250-821-28
C 33 155 37.3 17752 16 US-10-250-553-28
C 34 153 36.9 10078 13 US-10-033-190-3
C 35 146 35.2 831 9 US-09-794-384A-7
C 36 146 35.2 831 17 US-10-801-550-7
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C 38 122.6 29.5 9901 10 US-09-940-550A-11
C 39 117.6 28.3 11978 10 US-03-792-568-8
C 40 117.6 28.3 12438 10 US-03-792-568-9
C 41 101 24.3 694 9 US-09-733-151-39
C 42 101 24.3 694 15 US-10-375-332-39
C 43 97.4 23.5 909 9 US-09-733-151-36
C 44 97.4 23.5 909 15 US-10-375-332-36
C 45 57 13.7 69081 13 US-10-087-192-1192

ALIGNMENTS

RESULT 1

US-10-027-880-5/c
; Sequence 5, Application US/10027880
; Publication No. US20030106105A1
; GENERAL INFORMATION:
; APPLICANT: HOFFMAN, BEATE
; TITLE OF INVENTION: PROMOTER EXPRESSED SPECIFICALLY IN PLANT ROOT CELLS,
; TITLE OF INVENTION: VECTORS AND RECOMBINANT HOST CELLS CONTAINING SUCH A
; TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS OBTAINED
; FILE REFERENCE: CHEP-003US
; CURRENT APPLICATION NUMBER: US/10/027,880
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/FR00/01768
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7599
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T-DNA of pGKBs
US-10-027-880-5

Query Match 46.1%; Score 191.4; DB 15; Length 7599;
Best Local Similarity 99.5%; Pred. No. 6.6e-30;
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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6771 GATGTACATGGCGGATAAGAAAAGCAATTTCTAGATGTATTCCTATCTTTGAAGAAA 6712
Dd 283 TATAGTTTAAATATTTATTTATGATAAAATACAAAGTCAGGTATTTATGTCACAAACAAAACA 342
QY 6711 TATAGTTTAAATATTTATTTATGATAAAATACAAAGTCAGGTATTTATGTCACAAACAAAACA 6652
Dd

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:58:29 ; Search time 330.103 Seconds
(without alignments)
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Perfect score: 415
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	191.4	46.1	7599	15	US-10-027-880-5
C 2	188.8	45.5	6539	9	US-09-509-945-5
C 3	188.8	45.5	6548	9	US-09-509-945-4
C 4	188.4	45.4	4832	9	US-09-733-151-2
5	188.4	45.4	4832	15	US-10-375-332-2
6	188.4	45.4	4946	9	US-09-733-151-1
7	188.4	45.4	4946	15	US-10-375-332-1
8	188.4	45.4	5349	9	US-09-970-921-7
9	179.4	43.2	1077	9	US-09-733-151-24
10	179.4	43.2	1077	15	US-10-375-332-24
C 11	155	37.3	4465	13	US-10-047-542-13
C 12	155	37.3	6602	13	US-10-047-542-100


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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic
; OTHER INFORMATION: acid, "T-DNA of pTTS243"
; NAME/KEY: misc feature
; LOCATION: Complement(1)..(25)
; OTHER INFORMATION: label = RB, "T-DNA right border"
; NAME/KEY: misc feature
; LOCATION: Complement(98)..(331)
; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
; NAME/KEY: misc feature
; LOCATION: Complement(332)..(883)
; OTHER INFORMATION: label = bar, "region coding for phosphinthrincin
; OTHER INFORMATION: acetyl transferase"
; NAME/KEY: misc feature
; LOCATION: Complement(884)..(2258)
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
; OTHER INFORMATION: Virus"
; NAME/KEY: misc feature
; LOCATION: (2281)..(3969)
; OTHER INFORMATION: label = PE1, "promoter of E1 gene of rice (WO
; OTHER INFORMATION: 92/13956)"
; NAME/KEY: misc feature
; LOCATION: (3970)..(4245)
; OTHER INFORMATION: label = symb*, "improved barstar DNA"
; NAME/KEY: misc feature
; LOCATION: (4246)..(4577)
; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
; OTHER INFORMATION: end of chalcone synthase gene"
; NAME/KEY: misc feature
; LOCATION: Complement((5325)..(5349))
; OTHER INFORMATION: label = LB, "T-DNA left border"
;
US-09-970-921-7

Query Match 45.4%; Score 188.4; DB 9; Length 5349;
Best Local Similarity 99.5%; Pred. No. 2.5e-29;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 226 GTACATGCCGATAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATAT 285
Db 54 GTACATGTCGATAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATAT 113
QY 286 AGTTTAAATATTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAA 345
Db 114 AGTTTAAATATTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAA 173
QY 346 ATTATTGATGCAAGTTTAAATTCGAAATATTTCAATACTGATTATATCAGCTGGTAC 405
Db 174 ATTATTGATGCAAGTTTAAATTCGAAATATTTCAATACTGATTATATCAGCTGGTAC 233
QY 406 ATTGCCGTAG 415
Db 234 ATTGCCGTAG 243

RESULT 9
US-09-733-151-24
; Sequence 24, Application US/09733151
; Patent No. US20010029620A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1077)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
;
US-10-375-332-24
Query Match 43.2%; Score 179.4; DB 15; Length 1077;
Best Local Similarity 99.4%; Pred. No. 1.1e-27;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 CGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATATAGTTTAAAT 294
Db 880 CGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATATAGTTTAAAT 939
QY 295 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGA 354
Db 940 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGA 999
QY 355 TCGAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGGTACATTCGCCGTA 414
Db 1000 TCGAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGGTACATTCGCCGTA 1059
QY 415 G 415
Db 1060 G 1060

RESULT 10
US-10-375-332-24
; Sequence 24, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1077)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
;
US-10-375-332-24
Query Match 43.2%; Score 179.4; DB 15; Length 1077;
Best Local Similarity 99.4%; Pred. No. 1.1e-27;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 CGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATATAGTTTAAAT 294
Db 880 CGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATATAGTTTAAAT 939
QY 295 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGA 354
Db 940 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGA 999
QY 355 TCGAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGGTACATTCGCCGTA 414
Db 1000 TCGAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGGTACATTCGCCGTA 1059
QY 415 G 415
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; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1077)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
;
US-09-733-151-24

Query Match 43.2%; Score 179.4; DB 9; Length 1077;
Best Local Similarity 99.4%; Pred. No. 1.1e-27;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 CGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATATAGTTTAAAT 294
Db 880 CGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATATAGTTTAAAT 939
QY 295 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGA 354
Db 940 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGA 999
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Db 1000 TCGAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGGTACATTCGCCGTA 1059
QY 415 G 415
Db 1060 G 1060

RESULT 10
US-10-375-332-24
; Sequence 24, Application US/10375332
; Publication No. US20030188347A1
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REFERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/10/375,332
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/733,151
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1077)
; OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
;
US-10-375-332-24
Query Match 43.2%; Score 179.4; DB 15; Length 1077;
Best Local Similarity 99.4%; Pred. No. 1.1e-27;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 CGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATATAGTTTAAAT 294
Db 880 CGATAAGAAAGCAATTTGTAGATGTTAAATCCCATCTTGAAGAAATATAGTTTAAAT 939
QY 295 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGA 354
Db 940 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCCAAGCAAAACATAAATTTATTGA 999
QY 355 TCGAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGGTACATTCGCCGTA 414
Db 1000 TCGAAGTTTAAATTCAGAAATATTTCAATACTGATTATATCAGCTGGTACATTCGCCGTA 1059
QY 415 G 415
Db 1060 G 1060
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Db      1060 G 1060

RESULT 11
US-10-047-542-13/c
; Sequence 13, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; FILE REFERENCE: 030905.0004.CIPI
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 4465
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Expression-type plasmid pBMS-P-1
; NAME/KEY: modified_base
; LOCATION: (2150)
; OTHER INFORMATION: a, c, t or g
; NAME/KEY: modified_base
; LOCATION: (2214)..(2215)
; OTHER INFORMATION: a, c, t or g
US-10-047-542-13

Query Match      37.3%; Score 155; DB 13; Length 4465;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 TTAATTCCTTCCTGAAAGAAATATAGTTTAAATATTTTATTGATAAAATAACAAGTCAGG 320
DB      3733 TTAATTCCTTCCTGAAAGAAATATAGTTTAAATATTTTATTGATAAAATAACAAGTCAGG 3674

QY      321 TATTATAGTCCCAAGCAAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTTC 380
DB      3673 TATTATAGTCCCAAGCAAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTTC 3614

QY      381 AATACTGATTATATCAGCTGGTACATTCGCCGTAG 415
DB      3613 AATACTGATTATATCAGCTGGTACATTCGCCGTAG 3579

RESULT 12
US-10-047-542-100/c
; Sequence 100, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; FILE REFERENCE: 030905.0004.CIPI
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 6602
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:
; OTHER INFORMATION: PGTV-hpt-ocs-359J/SC
US-10-047-542-100

Query Match      37.3%; Score 155; DB 13; Length 7129;
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      261 TTAATTCCTTCCTGAAAGAAATATAGTTTAAATATTTTATTGATAAAATAACAAGTCAGG 320
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QY      321 TATTATAGTCCCAAGCAAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTTC 380
DB      793 TATTATAGTCCCAAGCAAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTTC 852

QY      381 AATACTGATTATATCAGCTGGTACATTCGCCGTAG 415
DB      853 AATACTGATTATATCAGCTGGTACATTCGCCGTAG 887

RESULT 14
US-10-047-542-14
; Sequence 14, Application US/10047542
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/ Publication No. US20020168367A1
/ GENERAL INFORMATION:
/ APPLICANT: LARRICK, JAMES W.
/ APPLICANT: WYCOFF, KEITH L.
/ TITLE OF INVENTION: NOVEL IMMUNOADRESINS FOR TREATING AND PREVENTING VIRAL
/ TITLE OF INVENTION: AND BACTERIAL DISEASES
/ FILE REFERENCE: 030905.0084.C1P1
/ CURRENT APPLICATION NUMBER: US/10/047,542
/ CURRENT FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: PCT/US01/13932
/ PRIOR FILING DATE: 2001-04-28
/ PRIOR APPLICATION NUMBER: 60/200,298
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 101
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 8074
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: Expression-type plasmid pMSP-1spJSC
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (2315)
/ OTHER INFORMATION: a, c, t or g
US-10-047-542-14

Query Match      37.3%; Score 155; DB 13; Length 8074;
Best Local Similarity 100.0%; Pred. No. 2.5e-22;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 TTAATTCCTCCAGCAAGCAATATAGTTTAAATATTTTATTGATAAATACCAAGTCAGG 320
DB 733 TTAATTCCTCCAGCAAGCAATATAGTTTAAATATTTTATTGATAAATACCAAGTCAGG 792

QY 321 TATTATAGTCCAGCAAGCAATATATTTATTGATGCAAGTTTAAATTCAGAAATATTTTC 380
DB 793 TATTATAGTCCAGCAAGCAATATATTTATTGATGCAAGTTTAAATTCAGAAATATTTTC 852

QY 381 AATACTGATTATATCAGCTGGTACATTGCCGTAG 415
DB 853 AATACTGATTATATCAGCTGGTACATTGCCGTAG 887

RESULT 15
US-09-847-057-4
/ Sequence 4, Application US/09847057
/ Patent No. US20020004943A1
/ GENERAL INFORMATION:
/ APPLICANT: AGRINOMICS, LLC.
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLAN
/ FILE REFERENCE: PAGODA
/ CURRENT APPLICATION NUMBER: US/09/847,057
/ CURRENT FILING DATE: 2001-05-01
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 8340
/ TYPE: DNA
/ ORGANISM: Binary vector pAG14002
US-09-847-057-4

Query Match      37.3%; Score 155; DB 9; Length 8340;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 TTAATTCCTCCAGCAAGCAATATAGTTTAAATATTTTATTGATAAATACCAAGTCAGG 320
DB 694 TTAATTCCTCCAGCAAGCAATATAGTTTAAATATTTTATTGATAAATACCAAGTCAGG 6553

QY 321 TATTATAGTCCAGCAAGCAATATATTTATTGATGCAAGTTTAAATTCAGAAATATTTTC 380
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Db 6554 TATTATAGTCCAGCAAGCAATATATTTATTGATGCAAGTTTAAATTCAGAAATATTTTC 6613
QY 381 AATACTGATTATATCAGCTGGTACATTGCCGTAG 415
DB 6614 AATACTGATTATATCAGCTGGTACATTGCCGTAG 6648

Search completed: December 5, 2004, 09:36:21
Job time : 331.103 secs
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